90489

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, April 01, 2003 12:31 PM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: Request for RUSH sequence search for 09/595526

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----
From: **Rao, Manjunath N.**
Sent: Tuesday, April 01, 2003 12:29 PM
To: Chan, Christina
Subject: Request for RUSH sequence search for 09/595526

Hello Christina,

Please authorize the request below as RUSH. The reason being this case is due soon and applicants have changed the sequence claims.

Thanks
Manjunath

10D01

From: Manjunath N. Rao ← deliver to
Art Unit 1652, Room 10A11
Mail Box in Room 10C 01?
Phone: 306-5681

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Date: 4-1-03

Please search the following as soon as possible for application with serial number **09/595,526 (Update)**

1. Nucleotides 1-500, 2250-2750, 4750-5250, 7250-7750, 9500-10,276 of SEQ ID NO:1
(total number of nucleotides to be searched= 2726)

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher: BOB	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up:	Bibliographic:	DRLink:
Date Completed: 4-4-03	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

90489

2. Nucleotides 291-7074 of SEQ ID NO:1 (total number of nucleotides=6784)

against all commercial nucleic acid databases including issued patents database and pending application database and provide **a print of all results.**

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Crystal Mall 1, USPTO.

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_____	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_____	Bibliographic:_____	DRLink:_____
Date Completed:_____	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_____
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 990.903 Seconds
(without alignments)
14684.987 Million cell updates/sec

Title: US-09-595-526C-1_COPY_1_500
Perfect score: 500
Sequence: 1 ggccgggacccgcagagccg.....caggaacacttccttgggtt 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		500	100.0	10442	6	AX060713	AX060713 Sequence
2		500	100.0	10442	6	AX060892	AX060892 Sequence
3		500	100.0	10442	9	AF285167	AF285167 Homo sapi
4		492.6	98.5	10474	6	AX060719	AX060719 Sequence
5		492.6	98.5	10474	6	AX060721	AX060721 Sequence
6		492.6	98.5	10474	6	AX060898	AX060898 Sequence
7		492.6	98.5	10474	6	AX060900	AX060900 Sequence
8		486.4	97.3	7260	6	AX253452	AX253452 Sequence
9		484.4	96.9	697	9	AF258627	AF258627 Homo sapi
10		483.2	96.6	9854	6	AX127831	AX127831 Sequence
11		483.2	96.6	9854	6	AX139818	AX139818 Sequence
12		481.6	96.3	1556	9	AK024328	AK024328 Homo sapi
13		378.2	75.6	446	6	AX127764	AX127764 Sequence
14		378.2	75.6	446	6	AX139751	AX139751 Sequence
15		378.2	75.6	9741	6	AX127830	AX127830 Sequence
16		378.2	75.6	9741	6	AX139817	AX139817 Sequence
17		378.2	75.6	9741	6	AX351038	AX351038 Sequence
18		283.4	56.7	298	9	AB037924	AB037924 Homo sapi
19		282.4	56.5	7860	6	AX092594	AX092594 Sequence
20		279.2	55.8	7862	6	AX135712	AX135712 Sequence
21		206.8	41.4	6786	9	AB055982	AB055982 Homo sapi
22		199.4	39.9	1167	9	AF258623S1	AF258623 Homo sapi
23		199.4	39.9	1167	9	HSA252201	AJ252201 Homo sapi
24		199.4	39.9	1750	9	AK022254	AK022254 Homo sapi
25		199.4	39.9	3231	6	AX351029	AX351029 Sequence
26	c	199.4	39.9	96717	9	AL359182	AL359182 Human DNA
27		199.4	39.9	149034	9	AF275948	AF275948 Homo sapi
28		199.4	39.9	175064	2	AC012230	AC012230 Homo sapi
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34		195.6	39.1	7878	10	MMABC1	X75926 Mus musculu
35	c	182.6	36.5	69570	2	AC021246	AC021246 Homo sapi
36		159.4	31.9	357	6	AX351030	AX351030 Sequence
37		155.8	31.2	159	6	AX351033	AX351033 Sequence
38		150	30.0	6880	6	AX253450	AX253450 Sequence
39		150	30.0	6880	9	HSA012376	AJ012376 Homo sapi
40		150	30.0	9495	6	AX059978	AX059978 Sequence
41		150	30.0	9497	6	AX059973	AX059973 Sequence
42		150	30.0	9497	9	AF165281	AF165281 Homo sapi
43		150	30.0	9593	6	AX059976	AX059976 Sequence
44		149	29.8	480	9	HSA252277	AJ252277 Homo sapi
45	c	149	29.8	129608	9	AL353685	AL353685 Human DNA

ALIGNMENTS

RESULT 1
AX060713
LOCUS AX060713 10442 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078972.
ACCESSION AX060713
VERSION AX060713.1 GI:12406103
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;

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          CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
                     /organism="Homo sapiens"
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BASE COUNT     2898 a   2297 c   2408 g   2835 t      4 others
ORIGIN

  Query Match             100.0%;  Score 500;  DB 6;  Length 10442;
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  Matches  500;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
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Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     481 CAGGAACACTTCCTTGGGTT 500


RESULT 2
AX060892
LOCUS       AX060892               10442 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078971.
ACCESSION   AX060892
VERSION     AX060892.1  GI:12406270
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 1 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2898 a   2297 c   2408 g   2835 t      4 others
ORIGIN

  Query Match             100.0%;  Score 500;  DB 6;  Length 10442;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-134;
  Matches  500;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
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Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     481 CAGGAACACTTCCTTGGGTT 500


RESULT 3
AF285167
LOCUS       AF285167               10442 bp    mRNA    linear   PRI 09-AUG-2000
DEFINITION  Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
            complete cds.
ACCESSION   AF285167
VERSION     AF285167.1  GI:9755158
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Schwartz,K., Lawn,R.M. and Wade,D.P.
  TITLE     ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
            regulated by LXR
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
            Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
            3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES             Location/Qualifiers
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BASE COUNT      2898 a    2297 c    2408 g    2835 t       4 others
ORIGIN

  Query Match           100.0%;  Score 500;  DB 9;  Length 10442;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-134;
  Matches  500;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
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Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     481 CAGGAACACTTCCTTGGGTT 500


RESULT 4
AX060719
LOCUS       AX060719               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078972.
ACCESSION   AX060719
VERSION     AX060719.1  GI:12406108
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 7 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      2906 a    2305 c    2416 g    2843 t       4 others
ORIGIN

  Query Match           98.5%;  Score 492.6;  DB 6;  Length 10474;
  Best Local Similarity  99.2%;  Pred. No. 1.8e-132;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
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Db      34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy      62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
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Db      94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy     122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
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Db     154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy     182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
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Db     214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy     242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy     302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy     362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy     422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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Db    454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy    482 AGGAACACTTCCTTGGGTT 500
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Db    514 AGGAACACTTCCTTGGGTT 532


RESULT 5
AX060721
LOCUS       AX060721               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 9 from Patent WO0078972.
ACCESSION   AX060721
VERSION     AX060721.1  GI:12406109
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2907 a    2304 c    2415 g    2844 t      4 others
ORIGIN

  Query Match           98.5%;  Score 492.6;  DB 6;  Length 10474;
  Best Local Similarity  99.2%;  Pred. No. 1.8e-132;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
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Db     34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy     62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
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Db     94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy    122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
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Db    154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy    182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
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Db    214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy    242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy    302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy    362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy    422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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Db    454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy    482 AGGAACACTTCCTTGGGTT 500
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Db    514 AGGAACACTTCCTTGGGTT 532


RESULT 6
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AX060898
LOCUS       AX060898               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078971.
ACCESSION   AX060898
VERSION     AX060898.1  GI:12406275
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 7 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2906 a    2305 c    2416 g    2843 t      4 others
ORIGIN

  Query Match           98.5%;  Score 492.6;  DB 6;  Length 10474;
  Best Local Similarity  99.2%;  Pred. No. 1.8e-132;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
          | |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy     62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy    122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy    182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
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Db    214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy    242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy    302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
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Db    334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy    362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy    422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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Db    454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy    482 AGGAACACTTCCTTGGGTT 500
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Db    514 AGGAACACTTCCTTGGGTT 532


RESULT 7
AX060900
LOCUS       AX060900               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 9 from Patent WO0078971.
ACCESSION   AX060900
VERSION     AX060900.1  GI:12406276
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2907 a    2304 c    2415 g    2844 t      4 others
ORIGIN

  Query Match             98.5%;  Score 492.6;  DB 6;  Length 10474;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-132;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
           | |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy      62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy     122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy     182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy     242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
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Db     274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy     302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
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Db     334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy     362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
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Db     394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy     422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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Db     454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy     482 AGGAACACTTCCTTGGGTT 500
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Db     514 AGGAACACTTCCTTGGGTT 532


RESULT 8
AX253452
LOCUS       AX253452                7260 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 3 from Patent WO0170810.
ACCESSION   AX253452
VERSION     AX253452.1  GI:16073979
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7260)
  AUTHORS   Schmitz,G. and Bodzioch,M.
  TITLE     Atp binding cassette transporter 1 (abc1) gene polymorphisms and
            uses thereof for the diagnosis and treatment of lipid,
            cardiovascular or inflammatory disorders
  JOURNAL   Patent: WO 0170810-A 3 27-SEP-2001;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .7260
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1834 a    1765 c    1905 g    1756 t
ORIGIN

  Query Match             97.3%;  Score 486.4;  DB 6;  Length 7260;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-130;
  Matches  498;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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Db      32 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 91

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 151

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 211

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     212 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 270

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
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Db     271 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 330

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 390

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
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Db     391 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 450

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db     451 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 510

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     511 CAGGAACACTTCCTTGGGTT 530


RESULT 9
AF258627
LOCUS       AF258627                697 bp    mRNA    linear   PRI 11-MAY-2000
DEFINITION  Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA,
            partial cds.
ACCESSION   AF258627
VERSION     AF258627.1  GI:7769707
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
            Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
  TITLE     Analysis of hABC1 gene 5' end: additional peptide sequence,
            promoter region, and four polymorphisms
  JOURNAL   Biochem. Biophys. Res. Commun. 271 (2000) In press
REFERENCE   2  (bases 1 to 697)
  AUTHORS   Pullinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C.,
            Aouizerat,B.E., Fielding,C.J. and Kane,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Cardiovascular Research Institute,
            University of California, San Francisco, 505 Parnassus Avenue, San
            Francisco, CA 94143-0130, USA
FEATURES             Location/Qualifiers
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                     /product="ATP binding cassette transporter 1"
                     /protein_id="AAF69513.1"
                     /db_xref="GI:7769708"
                     /translation="MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL
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BASE COUNT      152 a    198 c    190 g    156 t      1 others
ORIGIN

  Query Match             96.9%;  Score 484.4;  DB 9;  Length 697;
  Best Local Similarity   99.2%;  Pred. No. 3.5e-130;
  Matches  496;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Db     107 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 166

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
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Db     167 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 226

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
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Db     227 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 286

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     287 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 345

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
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Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
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Db     406 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 465

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
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Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db     526 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 585

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     586 CAGGAACACTTCCTTGGGTT 605


RESULT 10
AX127831
LOCUS       AX127831               9854 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 70 from Patent WO0130848.
ACCESSION   AX127831
VERSION     AX127831.1  GI:14134478
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9854)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 70 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9854
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2665 a    2219 c    2334 g    2635 t      1 others
ORIGIN

  Query Match             96.6%;  Score 483.2;  DB 6;  Length 9854;
  Best Local Similarity   99.2%;  Pred. No. 9.8e-130;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 68

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 128

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 188

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     189 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 247

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     248 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 307

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 367

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           |||||  | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 427

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 487

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     488 CAGGAACACTTCCTTGGGTT 507


RESULT 11
AX139818
LOCUS       AX139818               9854 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 70 from Patent EP1096012.
ACCESSION   AX139818
VERSION     AX139818.1  GI:14275400
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9854)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleics acids of the human abc1 gene and their therapeutic and
            diagnostic application
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  JOURNAL   Patent: EP 1096012-A 70 02-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9854
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2665 a    2219 c    2334 g    2635 t      1 others
ORIGIN
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Query Match 96.6%; Score 483.2; DB 6; Length 9854;
Best Local Similarity 99.2%; Pred. No. 9.8e-130;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
Db      69 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 128

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
Db     129 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 188

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
Db     189 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 247

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
Db     248 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 307

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
Db     308 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 367

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
Db     368 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 427

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db     428 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 487

Qy     481 CAGGAACACTTCCTTGGGTT 500
Db     488 CAGGAACACTTCCTTGGGTT 507
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RESULT 12
AK024328
LOCUS       AK024328               1556 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14266 fis, clone PLACE1002437, highly similar
            to ATP-BINDING CASSETTE TRANSPORTER 1.
ACCESSION   AK024328
VERSION     AK024328.1  GI:10436685
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
            clone:PLACE1002437.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
            Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
            Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
            Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1556)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing and clone selection:
            Helix Research Institute (supported by Japan Key Technology Center
            etc.) and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES             Location/Qualifiers
     source          1. .1556
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="PLACE1002437"
                     /tissue_type="placenta"
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                     /note="cloning vector: pME18SFL3"
     CDS             314. .1405
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                     NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
                     KEKLAAAERVLRSNMDILKPILMDVACDDIAHGQLTVPRSAAVAATGDAKPNMMGRET
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Query Match 96.3%; Score 481.6; DB 9; Length 1556;
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Matches 495; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
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Db     145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
Db     205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
Db     264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
Db     324 GGCCCCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
Db     384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db     444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy     481 CAGGAACACTTCCTTGGGTT 500
Db     504 CAGGAACACTTCCTTGGGTT 523
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RESULT 13
AX127764
LOCUS       AX127764                446 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3 from Patent WO0130848.
ACCESSION   AX127764
VERSION     AX127764.1  GI:14134411
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 3 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .446
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                     /db_xref="taxon:32630"
                     /note="Oligonucleotide Primer"
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  Best Local Similarity   99.0%;  Pred. No. 3.2e-99;
  Matches  391;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

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Db       1 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 60

Qy     166 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCT 225
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      61 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCT 119

Qy     226 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAG 285
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Db     120 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAG 179

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Qy     346 GAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 405
           |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db     240 GAAGACAAACATGTCAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 299

Qy     406 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 465
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Db     300 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 359

Qy     466 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 500
           |||||||||||||||||||||||||||||||||||
Db     360 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 394


RESULT 14
AX139751
LOCUS       AX139751                446 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1096012.
ACCESSION   AX139751
VERSION     AX139751.1  GI:14275333
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleics acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: EP 1096012-A 3 02-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /note="Oligonucleotide Primer"
BASE COUNT       96 a    123 c    112 g    115 t
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  Query Match             75.6%;  Score 378.2;  DB 6;  Length 446;
  Best Local Similarity   99.0%;  Pred. No. 3.2e-99;
  Matches  391;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     106 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 165
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Db       1 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 60

Qy     166 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCT 225
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Qy     226 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAG 285
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Db     120 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAG 179

Qy     286 GGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAA 345
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Qy     346 GAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 405
           |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db     240 GAAGACAAACATGTCAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 299

Qy     406 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 359

Qy     466 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 500
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Db     360 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 394


RESULT 15
AX127830
LOCUS       AX127830                9741 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 69 from Patent WO0130848.
ACCESSION   AX127830
VERSION     AX127830.1  GI:14134477
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9741)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 69 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2650 a   2180 c   2290 g   2620 t      1 others
ORIGIN
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Query Match 75.6%; Score 378.2; DB 6; Length 9741;
Best Local Similarity 99.0%; Pred. No. 4.2e-99;
Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy    106 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 165
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Db      1 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 60

Qy    166 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCT 225
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Db    120 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAG 179

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 GGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAA 239

Qy    346 GAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 405
          |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db    240 GAAGACAAACATGTCAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 299

Qy    406 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 359

Qy    466 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 500
          |||||||||||||||||||||||||||||||||||
Db    360 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 394
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	500	100.0	10442	22	AAF24680	Nucleotide sequenc
2	500	100.0	10442	22	AAF24702	Nucleotide sequenc
3	492.6	98.5	10474	22	AAF24685	Nucleotide sequenc
4	492.6	98.5	10474	22	AAF24686	Nucleotide sequenc
5	492.6	98.5	10474	22	AAF24707	Nucleotide sequenc
6	492.6	98.5	10474	22	AAF24708	Nucleotide sequenc
7	486.4	97.3	7260	22	AAD21326	Human ATP binding
8	486.4	97.3	7260	22	AAI70315	Human ATP binding
9	483.2	96.6	7086	22	ABA09200	Human ABCA1 homolo
10	483.2	96.6	7086	22	AAK52667	Human polynucleoti
11	483.2	96.6	7281	22	AAK51683	Human polynucleoti
12	483.2	96.6	9854	22	AAS06121	Human ABC1 DNA seq
13	481.6	96.3	736	22	AAH07432	Human cDNA clone (
14	481.6	96.3	1556	22	AAH18606	Human cDNA sequenc
15	378.2	75.6	446	22	AAS04035	Partial human ABC1
16	378.2	75.6	9741	22	AAS06120	Human ABC1 DNA seq
17	378.2	75.6	9741	24	AAD37273	Human ABC1 full-le
18	282.4	56.5	7857	21	AAC69388	Human ABC1 cholest
19	282.4	56.5	7860	22	AAF92835	Human ABC1 cDNA.
20	282.4	56.5	7861	21	AAC69387	Human ABC1 cholest
21	282.4	56.5	7864	21	AAC69120	Human ABC1 cholest
22	282.4	56.5	7864	21	AAC69385	Human ABC1 cholest
23	282.4	56.5	7864	21	AAC69386	Human ABC1 cholest
24	282.4	56.5	7864	21	AAC69389	Human ABC1 cholest
25	279.2	55.8	7860	22	AAF83826	Human ABC1 nucleot
26	199.4	39.9	763	22	AAH04729	Human cDNA clone (
27	199.4	39.9	1750	22	AAH17451	Human cDNA sequenc
28	199.4	39.9	3231	24	AAD37265	Human ABC1 transcr
29	199	39.8	183999	22	AAF92831	Human ABC1 genomic
30	197	39.4	221	24	AAD37268	Human ABC1 gene ex
31	173	34.6	227	21	AAC09615	Human secreted pro
32	159.4	31.9	357	24	AAD37266	Human ABC1 transcr
33	155.8	31.2	159	24	AAD37269	Human ABC1 gene ex
34	150	30.0	6880	21	AAZ94734	Human ATP binding
35	150	30.0	6880	22	AAD21325	Human ATP binding
36	150	30.0	6880	22	AAI70314	Human ATP binding
37	149	29.8	10545	21	AAC69132	Human ABC1 gene ex
38	100	20.0	534	21	AAC75311	Human ORFX ORF866
39	100	20.0	1133	22	AAD05589	Human secreted pro
40	100	20.0	6791	24	AAL44693	Human transporter
41	100	20.0	7795	24	ABL57810	Human ABCA7 coding
42	98.6	19.7	5669	22	AAS08707	Human PD-ATP-bindi
43	98.6	19.7	6522	22	AAS08706	Human PD-ATP-bindi
44	92	18.4	4736	21	AAC69133	Human ABC1 gene ex
45	92	18.4	11754	22	AAS04033	Human ABC1 gene, p

ALIGNMENTS

RESULT 1
AAF24680
ID AAF24680 standard; DNA; 10442 BP.
XX
AC AAF24680;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX

PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI; 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 122-128; 215pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 500; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
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Db      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
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Db     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180

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Db     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
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Db     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
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Db     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360

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Db     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480

Qy     481 CAGGAACACTTCCTTGGGTT 500
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Db     481 CAGGAACACTTCCTTGGGTT 500
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RESULT 2

AAF24702
ID AAF24702 standard; DNA; 10442 BP.
XX
AC AAF24702;.
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
DR P-PSDB; AAB31365.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Claim 3; Page 117-123; 211pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 500; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
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Db    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240

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Db    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
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Db    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480

Qy    481 CAGGAACACTTCCTTGGGTT 500
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Db    481 CAGGAACACTTCCTTGGGTT 500


RESULT 3
AAF24685
ID   AAF24685 standard; DNA; 10474 BP.
XX
AC   AAF24685;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag= a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 148-154; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

  Query Match             98.5%;  Score 492.6;  DB 22;  Length 10474;
  Best Local Similarity   99.2%;  Pred. No. 2.3e-142;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy    182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
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Qy    302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
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Qy    362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
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Qy    422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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RESULT 4
AAF24686
ID   AAF24686 standard; DNA; 10474 BP.
XX
AC   AAF24686;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 170-176; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match             98.5%;  Score 492.6;  DB 22;  Length 10474;
  Best Local Similarity   99.2%;  Pred. No. 2.3e-142;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
           | |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy      62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
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Qy     182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
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Qy     242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
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Db     274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy     302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy     362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
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Db     394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy     422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
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Db     454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy     482 AGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     514 AGGAACACTTCCTTGGGTT 532


RESULT 5
AAF24707
ID   AAF24707 standard; DNA; 10474 BP.
XX
AC   AAF24707;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31366.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 27; Page 144-150; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
```

CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
XX
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 98.5%; Score 492.6; DB 22; Length 10474;
Best Local Similarity 99.2%; Pred. No. 2.3e-142;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
           | |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy      62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy     122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy     182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy     242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333

Qy     302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy     362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy     422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy     482 AGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||
Db     514 AGGAACACTTCCTTGGGTT 532
```

RESULT 6
AAF24708
ID AAF24708 standard; DNA; 10474 BP.
XX
AC AAF24708;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 323..7108
FT /*tag= a
FT /product= "defective ABC1 polypeptide"
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
DR P-PSDB; AAB31367.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Claim 30; Page 165-172; 211pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
XX
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 98.5%; Score 492.6; DB 22; Length 10474;
Best Local Similarity 99.2%; Pred. No. 2.3e-142;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2 GCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 61
           | |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34 GGCACGAGCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGG 93

Qy      62 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 GAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCGG 153

Qy     122 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 TTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACA 213

Qy     182 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCT 273

Qy     242 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTG 333
```

```
Qy     302 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCA 393

Qy     362 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 GCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCT 453

Qy     422 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 GAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513

Qy     482 AGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     514 AGGAACACTTCCTTGGGTT 532
```

```
RESULT 7
AAD21326
ID   AAD21326 standard; DNA; 7260 BP.
XX
AC   AAD21326;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) gene.
XX
KW   Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
KW   dermatological; atherosclerosis; cardiovascular; inflammatory disease;
KW   psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
KW   immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..7106
FT                   /*tag=  a
FT                   /product= "Human ABC1 protein"
XX
PN   EP1136552-A1.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000EP-0105820.
XX
PR   20-MAR-2000; 2000EP-0105820.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640388/74.
DR   P-PSDB; AAE13022.
XX
PT   New adenosine triphosphate binding cassette transporter-1 gene
PT   polymorphisms, useful for diagnosing and treating lipid disorders,
PT   cardiovascular diseases and inflammatory diseases  -
XX
PS   Example 1; Fig 1; 48pp; English.
XX
CC   The invention relates to four common polymorphisms in the gene encoding
CC   ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with
CC   decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
CC   ABC1 directly affects cellular lipid homeostasis, which is a key factor
CC   in the atherogenetic processes. The ABC1 polymorphisms are useful for
CC   diagnosing and treating lipid disorders, cardiovascular diseases
CC   (coronary heart disease, atherosclerosis) and inflammatory diseases
CC   (psoriasis, lupus erythematosus). The identification of ABC1 as a
CC   transporter for interleukin-1beta (IL-1beta) identifies this gene as
CC   a candidate for treatment of inflammatory diseases including rheumatoid
CC   arthritis and septic shock. The present sequence is human ABC1 gene.
XX
```

```
SQ   Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

  Query Match             97.3%;  Score 486.4;  DB 22;  Length 7260;
  Best Local Similarity   99.6%;  Pred. No. 1.6e-140;
  Matches  498;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 91

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 151

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 211

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     212 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 270

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     271 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 330

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 390

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 450

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 510

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     511 CAGGAACACTTCCTTGGGTT 530
```

```
RESULT 8
AAI70315
ID   AAI70315 standard; cDNA; 7260 BP.
XX
AC   AAI70315;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) cDNA.
XX
KW   ATP binding cassette transporter 1; ABC1; human; lipid disorder;
KW   cholesterol; cardiovascular disease; inflammatory disease;
KW   antiinflammatory; antilipaemic; antipsoriatic; dermatological;
KW   Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW   polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..7106
FT                   /*tag=  a
FT   CDS             501..7106
FT                   /*tag=  b
FT                   /note= "alternative open reading frame of AAI70314"
FT   variation       replace(976,A)
FT                   /*tag=  c
FT   variation       replace(1516,C)
FT                   /*tag=  d
FT   variation       replace(2969,G)
FT                   /*tag=  e
```

```
FT   variation       replace(3836,C)
FT                   /*tag=  f
XX
PN   EP1136554-A1.
XX
PD   26-SEP-2001.
XX
PF   24-MAR-2000; 2000EP-0106401.
XX
PR   24-MAR-2000; 2000EP-0106401.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640389/74.
DR   P-PSDB; AAM50228.
XX
PT   New adenosine triphosphate binding cassette transporter gene
PT   polymorphisms, useful for diagnosing and treating lipid disorders,
PT   cardiovascular diseases and inflammatory diseases -
XX
PS   Disclosure; Page 26-28; 41pp; English.
XX
CC   The present sequence is that of cDNA encoding the human adenosine
CC   triphosphate (ATP) binding cassette transporter 1 (ABC1) protein
CC   (see AAM50227).  The sequence includes an extended open reading
CC   frame (ORF) to that provided by the sequence in AAI70314, using
CC   an alternative ATG codon as initiation codon and thereby adding an
CC   extra 40 N-terminal amino acids to the encoded ABC1 protein (see
CC   AAM50228).  The invention provides 4 common polymorphisms in the
CC   ABC1 gene.  These were identified by sequencing the ABC1 gene in
CC   different Tangier kindreds.  In the variant genes (numbering as in
CC   AAI70314), G is changed to A at position 596, T is changed to C at
CC   position 1136, A is changed to G at position 2589 or G is changed
CC   to C at position 3456, or any combination of these.  All of these
CC   polymorphisms alter the amino acid sequence of ABC1 and therefore
CC   may affect its function.  The 2 most common polymorphisms (G596A)
CC   and A2589G) are both associated with a decreased in vitro ApoA-I
CC   mediated efflux of cholesterol from mononuclear phagocytes, a
CC   feature typical of Tangier disease.  3 Of the variants (G596A,
CC   A2589G and G3456C) are significantly increased in a population of
CC   men having low high density lipoprotein-cholesterol levels and
CC   established coronary heart disease (CHD) relative to CHD-free
CC   control subjects.  The use of the provided ABC1 polymorphisms for
CC   the diagnosis and treatment of lipid disorders, cardiovascular
CC   diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC   erythematodes) is claimed.  Modulation of ABC1 transcripts or
CC   proteins by antisense or ribozyme technology or RNA decoys is also
CC   claimed.
XX
SQ   Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

  Query Match             97.3%;  Score 486.4;  DB 22;  Length 7260;
  Best Local Similarity   99.6%;  Pred. No. 1.6e-140;
  Matches  498;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 91

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 151

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 211

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     212 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 270

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     271 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 330

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 390

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 450

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 510

Qy     481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db     511 CAGGAACACTTCCTTGGGTT 530


RESULT 9
ABA09200
ID   ABA09200 standard; cDNA; 7086 BP.
XX
AC   ABA09200;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US03800.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   P-PSDB; ABB11956.
XX
PT   Human proteins and DNA encoding sequences useful for preventing,
PT   treating or ameliorating a medical condition in a mammalian subject
PT   e.g. arthritis and cancer -
XX
PS   Claim 1; Page 833-835; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
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CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention.
XX
SQ   Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

  Query Match             96.6%;  Score 483.2;  DB 22;  Length 7086;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-139;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 74

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 134

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     135 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 194

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     195 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 253

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     254 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 313

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 373

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 433

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 493

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     494 CAGGAACACTTCCTTGGGTT 513


RESULT 10
AAK52667
ID   AAK52667 standard; cDNA; 7086 BP.
XX
AC   AAK52667;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 2196.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79534.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 4558-4560; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

  Query Match             96.6%;  Score 483.2;  DB 22;  Length 7086;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-139;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db      15 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 74

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 134

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     135 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 194

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     195 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 253

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     254 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 313

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 373

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 433

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 493

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     494 CAGGAACACTTCCTTGGGTT 513
```

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RESULT 11
AAK51683
ID   AAK51683 standard; cDNA; 7281 BP.
XX
AC   AAK51683;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 228.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78550.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 1086-1096; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
```

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  Query Match             96.6%;  Score 483.2;  DB 22;  Length 7281;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-139;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 112

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     113 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 172

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 232

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     233 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 291

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     292 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 351

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 411

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 471

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 531

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     532 CAGGAACACTTCCTTGGGTT 551
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RESULT 12
AAS06121
ID   AAS06121 standard; cDNA; 9854 BP.
XX
AC   AAS06121;
XX
DT   12-SEP-2001  (first entry)
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XX
DE   Human ABC1 DNA sequence #2.
XX
KW   Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW   cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW   lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             298..7078
FT                   /*tag= a
FT                   /product= "Human ABC1 protein"
XX
PN   WO200130848-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-EP10886.
XX
PR   26-OCT-1999;   99EP-0402668.
PR   01-MAR-2000; 2000US-0186260.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Denefle P,  Rosier-Montus M,  Arnould-Reguigne I,  Prades C,  Naudin L;
PI   Lemoine C,  Duverger N,  Jaye M,  Searfoss GH,  Remaley A,  Brewer HB;
PI   Dean M;
XX
DR   WPI; 2001-316327/33.
DR   P-PSDB; AAU02176.
XX
PT   New human ABC1 nucleic acids and polypeptides for treating
PT   atherosclerosis, malaria and diabetes -
XX
PS   Claim 1; Page 209-213; 368pp; English.
XX
CC   The sequence represents the coding sequence #2 of human ABC1. The
CC   nucleic acid sequence, primers and probes derived from the ABC1 sequence,
CC   and polypeptides and vectors are useful for the prevention of
CC   atherosclerosis, in a subject affected by a dysfunction in the reverse
CC   transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC   useful for screening for an active ingredient for the prevention or
CC   treatment of a disease resulting from dysfunction in the reverse
CC   transport of cholesterol. The nucleic acids and polypeptides are also
CC   useful for treating and preventing cardiovascular and neurological
CC   pathologies, and other diseases e.g. Tangier disease, lecithin-
CC   cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ   Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;

  Query Match             96.6%;  Score 483.2;  DB 22;  Length 9854;
  Best Local Similarity   99.2%;  Pred. No. 1.9e-139;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 68

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 128

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 188

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     189 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 247

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     248 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 307

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 367

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 427

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 487

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     488 CAGGAACACTTCCTTGGGTT 507


RESULT 13
AAH07432
ID   AAH07432 standard; cDNA; 736 BP.
XX
AC   AAH07432;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:4267.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
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CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;

  Query Match             96.3%;  Score 481.6;  DB 22;  Length 736;
  Best Local Similarity   99.0%;  Pred. No. 1.7e-139;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 GGCCCCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
           ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy     481 CAGGAACACTTCCTTGGGTT 500
           ||||||||||||||||||||
Db     504 CAGGAACACTTCCTTGGGTT 523


RESULT 14
AAH18606
ID   AAH18606 standard; cDNA; 1556 BP.
XX
AC   AAH18606;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:18808.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;

  Query Match             96.3%;  Score 481.6;  DB 22;  Length 1556;
  Best Local Similarity   99.0%;  Pred. No. 2.4e-139;
  Matches  495;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 GGCCCCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
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Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
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Db    504 CAGGAACACTTCCTTGGGTT 523
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RESULT 15
AAS04035
ID AAS04035 standard; cDNA; 446 BP.
XX
AC AAS04035;
XX
DT 12-SEP-2001 (first entry)
XX
DE Partial human ABC1 cDNA sequence.
XX
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 185..438
FT /*tag= a
FT /product= "Human ABC1 protein, amino acids 1 to 60"
XX
PN WO200130848-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-EP10886.
XX
PR 26-OCT-1999; 99EP-0402668.
PR 01-MAR-2000; 2000US-0186260.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI Dean M;
XX
DR WPI; 2001-316327/33.
DR P-PSDB; AAU02176.
XX
PT New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX
PS Example 2; Page 167; 368pp; English.
XX
CC The sequence represents the partial coding sequence of human ABC1,
CC which encodes amino acids 1-60 of the human ABC1 protein. The nucleic
CC acid sequence, primers and probes derived from the ABC1 sequence, and
CC polypeptides and vectors are useful for the prevention of
CC atherosclerosis, in a subject affected by a dysfunction in the reverse
CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC useful for screening for an active ingredient for the prevention or
CC treatment of a disease resulting from dysfunction in the reverse
CC transport of cholesterol. The nucleic acids and polypeptides are also
CC useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
CC cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;

Query Match 75.6%; Score 378.2; DB 22; Length 446;
Best Local Similarity 99.0%; Pred. No. 2e-107;

Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy    106 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 165
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Db      1 CTTGTTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 60

Qy    166 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCT 225
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     61 GAAAGAGACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCT 119

Qy    226 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAG 285
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    120 GTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAG 179

Qy    286 GGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAA 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 GGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAA 239

Qy    346 GAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 405
          |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db    240 GAAGACAAACATGTCAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCC 299

Qy    406 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 TGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATA 359

Qy    466 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 500
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Db    360 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 394
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Search completed: April 3, 2003, 13:36:00
Job time : 91.2842 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.7495 Seconds
(without alignments)
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Title: US-09-595-526C-1_COPY_1_500
Perfect score: 500
Sequence: 1 ggccgggacccgcagagccg.....caggaacacttccttgggtt 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34.2	6.8	12537	2	US-08-611-280-4	Sequence 4, Appli
	2	34.2	6.8	12537	4	US-09-195-940-4	Sequence 4, Appli
	3	34.2	6.8	12537	4	US-09-562-466-4	Sequence 4, Appli
c	4	31.4	6.3	111282	4	US-09-754-250-3	Sequence 3, Appli
c	5	31.2	6.2	1006	4	US-08-988-242-17	Sequence 17, Appl
c	6	30.6	6.1	733	4	US-09-082-092-15	Sequence 15, Appl
	7	30.6	6.1	2875	3	US-08-458-434A-4	Sequence 4, Appli
	8	30.6	6.1	14636	4	US-09-173-914-6	Sequence 6, Appli
	9	30.2	6.0	454	4	US-08-998-416-84	Sequence 84, Appl
	10	30.2	6.0	1835	4	US-09-485-549-1	Sequence 1, Appli
	11	30.2	6.0	6525	3	US-08-762-500-74	Sequence 74, Appl
	12	29.8	6.0	5097	4	US-09-315-793-11	Sequence 11, Appl
c	13	29.6	5.9	987	4	US-09-370-838-289	Sequence 289, App
c	14	29.6	5.9	1146	1	US-08-482-385A-1	Sequence 1, Appli
c	15	29.6	5.9	2728	1	US-08-482-385A-5	Sequence 5, Appli
c	16	29.4	5.9	2067	2	US-08-713-928B-8	Sequence 8, Appli
c	17	29.4	5.9	2155	3	US-09-191-171-4	Sequence 4, Appli
c	18	29.4	5.9	2155	4	US-09-385-707-4	Sequence 4, Appli
c	19	29.4	5.9	2699	3	US-09-167-354-5	Sequence 5, Appli
c	20	29.4	5.9	2699	4	US-09-642-855-5	Sequence 5, Appli
c	21	29.4	5.9	2699	4	US-09-642-514-5	Sequence 5, Appli
	22	29.4	5.9	3627	2	US-08-232-087A-1	Sequence 1, Appli
c	23	29.4	5.9	4480	3	US-09-191-171-7	Sequence 7, Appli
c	24	29.4	5.9	4480	4	US-09-385-707-7	Sequence 7, Appli
c	25	29.4	5.9	6200	4	US-09-439-923-1	Sequence 1, Appli
c	26	29.2	5.8	4338	1	US-08-015-986A-1	Sequence 1, Appli
c	27	29.2	5.8	4338	2	US-08-446-363-1	Sequence 1, Appli
	28	29	5.8	1299	3	US-08-793-035-3	Sequence 3, Appli
	29	29	5.8	2754	4	US-09-429-322-3	Sequence 3, Appli
	30	29	5.8	3511	4	US-09-453-702B-187	Sequence 187, App
c	31	29	5.8	6176	3	US-08-911-321-6	Sequence 6, Appli
	32	28.8	5.8	1633	4	US-09-119-788-1	Sequence 1, Appli
	33	28.8	5.8	30001	1	US-08-125-468-1	Sequence 1, Appli
	34	28.8	5.8	30001	2	US-08-474-933-1	Sequence 1, Appli
	35	28.8	5.8	168575	4	US-09-426-290-1	Sequence 1, Appli
c	36	28.8	5.8	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	37	28.8	5.8	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	38	28.6	5.7	599	6	5430019-1	Patent No. 5430019
	39	28.6	5.7	2180	2	US-08-755-559-2	Sequence 2, Appli
	40	28.6	5.7	2180	3	US-09-210-474-2	Sequence 2, Appli
	41	28.6	5.7	2180	4	US-09-539-774-2	Sequence 2, Appli
c	42	28.6	5.7	2326	4	US-09-154-750A-76	Sequence 76, Appl
	43	28.6	5.7	15378	3	US-08-785-420-1	Sequence 1, Appli
	44	28.4	5.7	4771	2	US-08-866-650-2	Sequence 2, Appli
	45	28.4	5.7	4771	2	US-09-021-287-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-611-280-4
; Sequence 4, Application US/08611280
; Patent No. 5891666
; GENERAL INFORMATION:
; APPLICANT: Matsuyama, Toshifumi
; APPLICANT: Grossman, Alex
; APPLICANT: Richardson, Christopher D.
; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Canada Inc.
; STREET: 6733 Mississauga Road, Suite 303
; CITY: Mississauga
; STATE: Ontario
; COUNTRY: Canada
; ZIP: L5N 6JB
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,280
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-338A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-611-280-4

Query Match 6.8%; Score 34.2; DB 2; Length 12537;
Best Local Similarity 55.5%; Pred. No. 1.2;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy    296 TTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAAC 355
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Qy    356 ATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTG 414
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Db     82 TGTGAGGCTGGTGGCAGAGGAAGCCTGGCTTCCATCTCTGAGCCTGAGGGAGAATGCTG 140
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RESULT 2
US-09-195-940-4
; Sequence 4, Application US/09195940
; Patent No. 6258935
;  GENERAL INFORMATION:
;    APPLICANT:  Matsuyama, Toshifumi
;    APPLICANT:  Grossman, Alex
;    APPLICANT:  Richardson, Christopher D.
;    TITLE OF INVENTION:  NOVEL GENES ENCODING LSIRF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Canada Inc.
;      STREET:  6733 Mississauga Road, Suite 303
;      CITY:  Mississauga
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  L5N 6JB
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/195,940
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/611,280
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oleski, Nancy A.
;      REGISTRATION NUMBER:  34,688
;      REFERENCE/DOCKET NUMBER:  A-338A
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12537 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-195-940-4

  Query Match             6.8%;  Score 34.2;  DB 4;  Length 12537;
  Best Local Similarity   55.5%;  Pred. No. 1.2;
  Matches   66;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy     296 TTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAAC 355
           ||| || |||||||| ||  ||| | || || |   |||    |   | |||||    |
Db      22 TTGCTGCCCTCAGCTAAGAGTGCGGGTGAGGTAAGGCCTGTAGTCGGGCAGAAGGAGGAG 81

Qy     356 ATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTG 414
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RESULT 3
US-09-562-466-4
; Sequence 4, Application US/09562466
; Patent No. 6369202
;   GENERAL INFORMATION:
;        APPLICANT: Matsuyama, Toshifumi
;                   Grossman, Alex
;                   Richardson, Christopher D.
;        TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Canada Inc.
;             STREET: 6733 Mississauga Road, Suite 303
;             CITY: Mississauga
;             STATE: Ontario
;             COUNTRY: Canada
;             ZIP: L5N 6JB
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/562,466
;             FILING DATE: 01-May-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/195,940
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Oleski, Nancy A.
;             REGISTRATION NUMBER: 34,688
;             REFERENCE/DOCKET NUMBER: A-338A
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 12537 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-562-466-4

  Query Match             6.8%;  Score 34.2;  DB 4;  Length 12537;
  Best Local Similarity   55.5%;  Pred. No. 1.2;
  Matches   66;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy     296 TTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAAC 355
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Db      22 TTGCTGCCCTCAGCTAAGAGTGCGGGTGAGGTAAGGCCTGTAGTCGGGCAGAAGGAGGAG 81

Qy     356 ATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTG 414
             ||||  |    || |  ||||||| || || | |   |||||    ||   |||
Db      82 TGTGAGGCTGGTGGCAGAGGAAGCCTGGCTTCCATCTCTGAGCCTGAGGGAGAATGCTG 140


RESULT 4
US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui et al
;  TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
;  TITLE OF INVENTION:  PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001063
;  CURRENT APPLICATION NUMBER: US/09/754,250
;  CURRENT FILING DATE:  2001-01-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 111282
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(111282)
;   OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

  Query Match             6.3%;  Score 31.4;  DB 4;  Length 111282;
  Best Local Similarity   67.7%;  Pred. No. 29;
  Matches   44;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

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Db  38808 TCCGGGGATTCAGCGGGTCACCGGGGTCAGCTCCCTGCCCGGACCGACCCGGTTCTTAGG 38749

Qy      95 GCGCT 99
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Db  38748 CCTCT 38744


RESULT 5
US-08-988-242-17/c
; Sequence 17, Application US/08988242
; Patent No. 6403103
;  GENERAL INFORMATION:
;    APPLICANT:  PARANHOS-BACCALA, GLAUCIA
;    APPLICANT:  LESENECHAL, MYLENE
;    APPLICANT:  JOLIVET, MICHEL
;    APPLICANT:  MANDRAND, BERNARD
;    TITLE OF INVENTION:  NEW TRYPANOSOMA CRUZI ANTIGEN, GENE
;    TITLE OF INVENTION:  ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
;    TITLE OF INVENTION:  CHAGAS DISEASE
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE, PLC
;      STREET:  P.O. BOX 19928
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,242
;      FILING DATE:  10-DEC-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 36400A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1006 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-988-242-17

  Query Match             6.2%;  Score 31.2;  DB 4;  Length 1006;
  Best Local Similarity   55.6%;  Pred. No. 2.9;
  Matches   60;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy     114 TTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGA 173
           | | ||  |||| | |    |  ||||||| ||   |    ||  ||  ||| | | | |
Db     357 TCCGCCCCTTCTCTCTCTCTCTTTTCTCCGCAAAAATAAATAAAAGGGTGGAAACACAAA 298

Qy     174 CGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCC 221
           | || ||||||||    ||||     || ||| |  |    || ||||
Db     297 CACACACACAAAAAAAAAAAAGGAAAAAGGACAAATCTGACGCCTCCC 250


RESULT 6
US-09-082-092-15/c
; Sequence 15, Application US/09082092
; Patent No. 6251628
;  GENERAL INFORMATION:
;    APPLICANT:  Nakao, Atsuhito
;    APPLICANT:  Moren, Anita
;    APPLICANT:  Heuchel, Rainer
;    APPLICANT:  Itoh, Susumu
;    APPLICANT:  Afrakhte, Mozghan
;    APPLICANT:  Souchelnytskyi, Serhiy
;    APPLICANT:  Brodin, Greger
;    APPLICANT:  Landstrom, Marene
;    APPLICANT:  Heldin, Nils-Erik
;    APPLICANT:  Heldin, Carl-Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,092
;      FILING DATE:  20-MAY-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,221
;      FILING DATE:  20-MAY-1997
;      APPLICATION NUMBER:  60/060,465
;      FILING DATE:  30-SEP-1997
;      APPLICATION NUMBER:  60/075,940
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  60/077,033
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  733 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-082-092-15

  Query Match             6.1%;  Score 30.6;  DB 4;  Length 733;
  Best Local Similarity   60.0%;  Pred. No. 3.8;
  Matches   51;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy     217 GTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTG 276
           | | | |||| | ||||    ||| ||  ||  || |||| | |||   |||| ||||
Db     717 GCCGCCGCTGGGGGCTCGCCGCGCCGCACTCAGGGACTCCGGGGCCGAGCGCTCGGCGGC 658

Qy     277 CTGGCTGAGGGAACATGGCTTGTTG 301
           ||||   ||     ||||| | ||
Db     657 GTGGCGCCGGCTGGCTGGCTGGCTG 633


RESULT 7
US-08-458-434A-4
; Sequence 4, Application US/08458434A
; Patent No. 6083690
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Stephen E.
;    APPLICANT:  Mundy M.D., Gregory R.
;    APPLICANT:  Gosh-Choudhury Ph.D., Nandini
;    APPLICANT:  Feng Ph.D., Jian Q.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR IDENTIFYING
;    TITLE OF INVENTION:  OSTEOGENIC AGENTS
;    NUMBER OF SEQUENCES:  13
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James C. Weseman, Esq.
;      STREET:  401 B. Street, Suite 1700
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,434A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weseman, James C.
;      REGISTRATION NUMBER:  30,507
;      REFERENCE/DOCKET NUMBER:  P00060US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 699-3604
;      TELEFAX:  619-236-1048
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2875 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-458-434A-4

  Query Match             6.1%;  Score 30.6;  DB 3;  Length 2875;
  Best Local Similarity   48.6%;  Pred. No. 7.7;
  Matches   84;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy     139 CTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACACAAAAGTGGAAAACAGT 198
           || |  |  ||  | |  ||  | | ||     |||| |  | |   ||  || | |||
Db    2030 CTTCCCACAGCCCGCCCGGGATTGGCAGCCCCGGACGTAGCCTCCCCAGGCGACACCAGG 2089

Qy     199 TAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCG 258
           |  |    |||       |      |  | |||       |||| || |    || ||  |
Db    2090 CACCGGGACGCCCTCCCGGCGAAAGACGCGAGGGTCACCCGCGGCTTCGAGGGACTGGCA 2149

Qy     259 AGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTG 311
           | |||  | |||   | | | ||| | |  | ||||    |||||| ||||
Db    2150 CGACACGGGTTGGAACTCCAGACTGTGCGCGCCTGGCGCTGTGGCCTCGGCTG 2202


RESULT 8
US-09-173-914-6
; Sequence 6, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
;  APPLICANT: Hendrickson, Eric
;  TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
;  TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
;  FILE REFERENCE: B0877/7017/HK
;  CURRENT APPLICATION NUMBER: US/09/173,914
;  CURRENT FILING DATE: 1998-10-16
;  EARLIER APPLICATION NUMBER: 60/064,557
;  EARLIER FILING DATE: 1997-10-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 14636
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-173-914-6

  Query Match             6.1%;  Score 30.6;  DB 4;  Length 14636;
  Best Local Similarity   53.8%;  Pred. No. 18;
  Matches   63;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy     112 TTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGA 171
           || |||  | ||||  ||  | || |      |  ||| | |||  || |  | || |
Db     471 TTGTCCATGTTTCTCATTATTTCCTTAGAAATTACTTCTTCTAAAGAAGTTGCTGCAACA 530

Qy     172 GACGCAAACACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTG 228
           |||   |||| || || ||||   |  ||  || | ||   ||| |   |||   ||
Db     531 GACAGCAACAAAACAGGGGAAGGAATGTAGGGAGCTGCGGTGGGGGAAGCTGAGATG 587


RESULT 9
US-08-998-416-84
; Sequence 84, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1027RP
US-08-998-416-84

  Query Match             6.0%;  Score 30.2;  DB 4;  Length 454;
  Best Local Similarity   56.6%;  Pred. No. 3.9;
  Matches   56;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy     370 TGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCTGAGCTACC 429
           | || ||   ||||| | | ||  |||| | | |  || | | || ||||  ||
Db       5 TCGACGTACTCTGGCGTTTGTTCTTCTTCGTCAGCAGGAACGCCGTCCGGCATAGGCTTA 64

Qy     430 CACCCTATGAACAACATGAATGCCATTTTCCAAATAAAG 468
           |   || | |   |||||| |    |  | ||| |||||
Db      65 CTGACTTTCACAGACATGATTCTTTTGCTGCAAGTAAAG 103
```

```
RESULT 10
US-09-485-549-1
; Sequence 1, Application US/09485549
; Patent No. 6361948
; GENERAL INFORMATION:
;  APPLICANT:  James Tricoli
;  APPLICANT:  Rachel Rhondinelli
;  APPLICANT:  Fox Chase Cancer Center
;  TITLE OF INVENTION:  Prognostic Compositions for Prostate Cancer and Methods of Use
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:  FCCC 96-13
;  CURRENT APPLICATION NUMBER: US/09/485,549
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:  PCT/US98/16768
;  PRIOR FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER:  60/055,285
;  PRIOR FILING DATE:  1997-08-13
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1835
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-485-549-1

  Query Match             6.0%;  Score 30.2;  DB 4;  Length 1835;
  Best Local Similarity   53.9%;  Pred. No. 8.2;
  Matches   62;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           | ||  |||| || | ||||||  |   | ||| |||||     ||   |||   | ||
Db    1039 GCCCACGACCTGCCGCGCCGAGGAGCGGCATCTGTCCCGTTCCCGATTGGGTCTGTCGT 1098

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTT 115
             ||||||  | | |||||  |  |       | | || ||||  ||  || |
Db    1099 CTCTCTCCGCCTAGCGACAGATTCCTTCTATTAAGGGATTGGCTCGCTGAGTTCT 1153


RESULT 11
US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
;    APPLICANT:  Klinger, Katherine W.
;    TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;    TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/762,500
;      FILING DATE:  09-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,259
;      FILING DATE:  17-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10469
;      FILING DATE:  17-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-9.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 872-8400
;      TELEFAX:  (508) 872-5415
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6525 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  573..5684
US-08-762-500-74

  Query Match             6.0%;  Score 30.2;  DB 3;  Length 6525;
  Best Local Similarity   50.3%;  Pred. No. 16;
  Matches   74;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy     277 CTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCA 336
           ||  | |   ||  ||||||         ||||||  | | || || |||||||||  ||
Db     559 CTTTCAGCAAGACGATGGCTGTGCTCAGGCAGCTGGCGCTCCTCCTCTGGAAGAACTACA 618

Qy     337 CTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCT 396
           |  |    |   | |          |  | | ||||||  |   |  |||  |  | | |
Db     619 CCCTGCAGAAGCGGAAGGTCCTGGTGACGGTCCTGGAACTCTTCCTGCCATTGCTGTTTT 678

Qy     397 TCCTGATCCTGATCTCTGTTCGGCTGA 423
               |||||| ||||   | ||  |||
Db     679 CTGGGATCCTCATCTGGCTCCGCTTGA 705


RESULT 12
US-09-315-793-11
; Sequence 11, Application US/09315793
; Patent No. 6221597
; GENERAL INFORMATION:
;  APPLICANT: Roberts, Christopher J.
;  TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
;  TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
;  TITLE OF INVENTION: DRUGS
;  FILE REFERENCE: 9301-048
;  CURRENT APPLICATION NUMBER: US/09/315,793
;  CURRENT FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 5097
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-315-793-11

  Query Match             6.0%;  Score 29.8;  DB 4;  Length 5097;
  Best Local Similarity   51.9%;  Pred. No. 19;
  Matches   67;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy     129 TTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACACAAAAGT 188
           || | || || || | |   |||||  || |     ||| |  |        | |||||
Db    3050 TTTTACCATTGTCTGCATCTCTTGTACAGTGTGTTCAGAGATTGTTTTTGCTAGAAAAGA 3109

Qy     189 GGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCC 248
           |  ||   | | || |||| |||   || |  || ||| | | |||||  |    ||
Db    3110 GAGAAGGTGGTTATTACCAACCAATAGCTTTGCTTCTGGGTGGTCTGGAAGAGCTATTAG 3169

Qy     249 AGGGCTCCC 257
           ||   || |
```

```
Db   3170 AGATTTCAC 3178


RESULT 13
US-09-370-838-289/c
; Sequence 289, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Mohamath, Roadoh
;  APPLICANT: Secrist, Heather
;  TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;  TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.475C1
;  CURRENT APPLICATION NUMBER: US/09/370,838
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: US 09/285,323
;  EARLIER FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 289
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-370-838-289

  Query Match             5.9%;  Score 29.6;  DB 4;  Length 987;
  Best Local Similarity   53.4%;  Pred. No. 9.2;
  Matches   62;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy      51 GGCAGGGCGGGGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGT 110
           || ||   ||||      |  |||   |   ||| |||| |  | ||||||  |||||  |
Db     468 GGAAGATGGGGGCAAGAAGATCACGCTCCCCGCCTGTTCCCCCGCCGCTTTTCTCCTCTT 409

Qy     111 TTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAG 166
           |  |  |   |||||    || |||  || ||  |   |  | |   ||| ||| |
Db     408 TCCTCTCTTTGTTCTCAGCTCCCCCTGTCCCCTCAGCTCCAGACGTAGGGGAGGGG 353


RESULT 14
US-08-482-385A-1/c
; Sequence 1, Application US/08482385A
; Patent No. 5728561
;  GENERAL INFORMATION:
;    APPLICANT:  DENOYA,, CLAUDIO D.
;    TITLE OF INVENTION:  GENES ENCODING BRACHED CHAIN ALPHA
;    TITLE OF INVENTION:  KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER C. RICHARDSON
;      STREET:  235 EAST 42ND STREET, 20TH FLOOR
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A
;      ZIP:  10017-5755
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,385A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SHEYKA,, ROBERT F.
;      REGISTRATION NUMBER:  31,304
;      REFERENCE/DOCKET NUMBER:  PC8346C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-573-1189
;      TELEFAX:  212-573-1939
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1146 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-482-385A-1

  Query Match             5.9%;  Score 29.6;  DB 1;  Length 1146;
  Best Local Similarity   56.0%;  Pred. No. 9.9;
  Matches   56;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy     212 CGGGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGG 271
           ||| | | | || || ||||  |||||   |  ||  || |    |    |||  |||
Db     224 CGGCCCTGCTTGGTGAGAGCCGTGGCCTGCGTGTTGTAGCGGCGGCCGCGCACCAGCTCC 165

Qy     272 GCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTG 311
           |||| | ||| | |      | ||  || ||||||  || |
Db     164 GCGTACAGGCGGCGCAGCAGTAGCGGGTCGGCCTCCGCGG 125


RESULT 15
US-08-482-385A-5/c
; Sequence 5, Application US/08482385A
; Patent No. 5728561
;  GENERAL INFORMATION:
;    APPLICANT:  DENOYA,, CLAUDIO D.
;    TITLE OF INVENTION:  GENES ENCODING BRACHED CHAIN ALPHA
;    TITLE OF INVENTION:  KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER C. RICHARDSON
;      STREET:  235 EAST 42ND STREET, 20TH FLOOR
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A
;      ZIP:  10017-5755
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,385A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SHEYKA,, ROBERT F.
;      REGISTRATION NUMBER:  31,304
;      REFERENCE/DOCKET NUMBER:  PC8346C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-573-1189
;      TELEFAX:  212-573-1939
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2728 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-482-385A-5

  Query Match             5.9%;  Score 29.6;  DB 1;  Length 2728;
  Best Local Similarity   56.0%;  Pred. No. 16;
  Matches   56;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy     212 CGGGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGG 271
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Db     626 CGGCCCTGCTTGGTGAGAGCCGTGGCCTGCGTGTTGTAGCGGCGGCCGCGCACCAGCTCC 567

Qy     272 GCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTG 311
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Db     566 GCGTACAGGCGGCGCAGCAGTAGCGGGTCGGCCTCCGCGG 527
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Search completed: April 3, 2003, 13:09:48
Job time : 79.7495 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 31.629 Seconds
(without alignments)
13866.500 Million cell updates/sec

Title: US-09-595-526C-1_COPY_1_500
Perfect score: 500
Sequence: 1 ggccgggacccgcagagccg.....caggaacacttccttgggtt 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	483.2	96.6	9870	9	US-09-984-827-93	Sequence 93, Appl
2	483.2	96.6	9870	9	US-09-984-827-94	Sequence 94, Appl
3	483.2	96.6	9870	9	US-09-984-827-95	Sequence 95, Appl
4	483.2	96.6	9870	9	US-09-984-827-96	Sequence 96, Appl
5	483.2	96.6	9870	9	US-09-984-827-97	Sequence 97, Appl
6	483.2	96.6	9870	9	US-09-984-827-98	Sequence 98, Appl
7	483.2	96.6	9870	9	US-09-984-827-99	Sequence 99, Appl
8	483.2	96.6	9870	9	US-09-984-827-100	Sequence 100, App
9	483.2	96.6	9870	9	US-09-984-827-101	Sequence 101, App
10	483.2	96.6	9870	9	US-09-984-827-102	Sequence 102, App
11	483.2	96.6	9870	9	US-09-984-827-103	Sequence 103, App
12	483.2	96.6	9870	9	US-09-984-827-104	Sequence 104, App
13	483.2	96.6	9870	9	US-09-984-827-105	Sequence 105, App
14	483.2	96.6	9870	9	US-09-984-827-106	Sequence 106, App
15	483.2	96.6	9870	9	US-09-984-827-107	Sequence 107, App
16	483.2	96.6	9870	9	US-09-984-827-108	Sequence 108, App
17	483.2	96.6	9870	9	US-09-984-827-109	Sequence 109, App
18	483.2	96.6	9870	9	US-09-984-827-110	Sequence 110, App
19	483.2	96.6	9870	9	US-09-984-827-111	Sequence 111, App
20	483.2	96.6	9870	9	US-09-984-827-112	Sequence 112, App
21	483.2	96.6	9870	9	US-09-984-827-113	Sequence 113, App
22	483.2	96.6	9870	9	US-09-984-827-114	Sequence 114, App
23	483.2	96.6	9870	9	US-09-984-827-115	Sequence 115, App
24	483.2	96.6	9870	9	US-09-984-827-116	Sequence 116, App
25	483.2	96.6	9870	9	US-09-984-827-117	Sequence 117, App
26	483.2	96.6	9870	9	US-09-984-827-118	Sequence 118, App
27	483.2	96.6	9870	9	US-09-984-827-119	Sequence 119, App
28	483.2	96.6	9870	9	US-09-984-827-120	Sequence 120, App
29	483.2	96.6	9870	9	US-09-984-827-121	Sequence 121, App
30	483.2	96.6	9870	9	US-09-984-827-122	Sequence 122, App
31	483.2	96.6	9870	9	US-09-984-827-123	Sequence 123, App
32	483.2	96.6	9870	9	US-09-984-827-124	Sequence 124, App
33	483.2	96.6	9870	9	US-09-984-827-125	Sequence 125, App
34	483.2	96.6	9870	9	US-09-984-827-126	Sequence 126, App
35	481.6	96.3	9870	9	US-09-984-827-92	Sequence 92, Appl
36	378.2	75.6	9741	9	US-09-984-827-1	Sequence 1, Appli
37	378.2	75.6	9741	10	US-09-846-456-10	Sequence 10, Appl
38	289.2	57.8	1062	9	US-09-924-340-101	Sequence 101, App
39	289.2	57.8	1062	9	US-09-992-600A-101	Sequence 101, App
40	199.4	39.9	3231	9	US-09-984-827-3	Sequence 3, Appli
41	199.4	39.9	3231	10	US-09-846-456-1	Sequence 1, Appli
42	197	39.4	221	10	US-09-846-456-4	Sequence 4, Appli
43	195.4	39.1	221	9	US-09-984-827-24	Sequence 24, Appl
44	159.4	31.9	357	9	US-09-984-827-4	Sequence 4, Appli
45	159.4	31.9	357	10	US-09-846-456-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-984-827-93
; Sequence 93, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-93

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144
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Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
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Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
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Db    504 CAGGAACACTTCCTTGGGTT 523
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RESULT 2
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-94

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
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Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144
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Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
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Db    504 CAGGAACACTTCCTTGGGTT 523
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RESULT 3
US-09-984-827-95
; Sequence 95, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-95

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
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Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 4
US-09-984-827-96
; Sequence 96, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-96

  Query Match            96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity  99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 5
US-09-984-827-97
; Sequence 97, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-97

  Query Match            96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity  99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204
```

```
Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          |||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523
```

RESULT 6
US-09-984-827-98
; Sequence 98, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-98

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204
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Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          |||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523
```

RESULT 7
US-09-984-827-99
; Sequence 99, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-99

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
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```
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 8
US-09-984-827-100
; Sequence 100, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-100

  Query Match             96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity   99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 9
US-09-984-827-101
; Sequence 101, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-101

  Query Match             96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity   99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263
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```
Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 10
US-09-984-827-102
; Sequence 102, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-102

  Query Match             96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity   99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 11
US-09-984-827-103
; Sequence 103, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-103

  Query Match             96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity   99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
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```
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 12
US-09-984-827-104
; Sequence 104, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-104

  Query Match            96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity  99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
Db    504 CAGGAACACTTCCTTGGGTT 523


RESULT 13
US-09-984-827-105
; Sequence 105, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-105

  Query Match            96.6%;  Score 483.2;  DB 9;  Length 9870;
  Best Local Similarity  99.2%;  Pred. No. 7.5e-153;
  Matches  496;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323
```

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Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523
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RESULT 14
US-09-984-827-106
; Sequence 106, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-106

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323
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Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523
```

RESULT 15
US-09-984-827-107
; Sequence 107, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-107

Query Match 96.6%; Score 483.2; DB 9; Length 9870;
Best Local Similarity 99.2%; Pred. No. 7.5e-153;
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
Qy      1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

Qy     61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

Qy    121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

Qy    181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

Qy    241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

Qy    301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

Qy    361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

Qy    421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

Qy    481 CAGGAACACTTCCTTGGGTT 500
          ||||||||||||||||||||
Db    504 CAGGAACACTTCCTTGGGTT 523


Search completed: April  4, 2003, 06:41:22
Job time : 42.629 secs
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 565.192 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_1_500
Perfect score: 500
Sequence: 1 ggccgggacccgcagagccg.....caggaacacttccttgggtt 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	485.8	97.2	547	9	AL698654	AL698654 DKFZp686N
	2	481.6	96.3	736	9	AU135588	AU135588 AU135588
	3	268.4	53.7	292	14	Z44377	Z44377 HSC12B081 n
	4	264.8	53.0	619	10	BB657864	BB657864 BB657864
	5	254.8	51.0	535	12	BG384217	BG384217 303216 MA
	6	199.4	39.9	763	9	AU121731	AU121731 AU121731
	7	198	39.6	1004	11	BC034824	BC034824 Homo sapi
	8	178	35.6	998	12	BG678861	BG678861 602624760
	9	100	20.0	575	13	BI541694	BI541694 455529 MA
	10	92	18.4	335	10	AW313960	AW313960 9668 MARC
	11	88.6	17.7	470	17	BH042929	BH042929 RPCI-24-2
	12	87.2	17.4	370	14	BM691885	BM691885 UI-E-CL1-
	13	87.2	17.4	522	9	AL712499	AL712499 DKFZp686H
	14	87.2	17.4	523	9	AL712388	AL712388 DKFZp686L
	15	87.2	17.4	562	9	AL712461	AL712461 DKFZp686D
	16	85.6	17.1	462	9	AL713392	AL713392 DKFZp686G
	17	85.6	17.1	492	9	AL712362	AL712362 DKFZp686I
	18	82.2	16.4	315	12	BF721262	BF721262 mab64g11.
	19	73.4	14.7	259	10	BB594265	BB594265 BB594265
	20	73.4	14.7	272	10	BB568993	BB568993 BB568993
	21	68.6	13.7	365	10	BB843149	BB843149 BB843149
	22	67.4	13.5	276	10	BB570397	BB570397 BB570397
	23	65.8	13.2	547	17	AZ769996	AZ769996 1M0571A17
	24	65.8	13.2	625	10	BB665939	BB665939 BB665939
	25	58.4	11.7	265	14	BM940929	BM940929 UI-M-CG0p
c	26	58	11.6	243	12	BF455614	BF455614 UI-M-CG0p
	27	53.6	10.7	218	10	BB594197	BB594197 BB594197
	28	50.6	10.1	344	13	BM149133	BM149133 TCAAP2E63
c	29	45.2	9.0	694	14	BQ597641	BQ597641 MI-P-A2-a
	30	45	9.0	1054	13	BM544515	BM544515 AGENCOURT
c	31	41	8.2	533	10	AV845237	AV845237 AV845237
	32	40.8	8.2	914	17	CNS03WB8	AL263501 Tetraodon
	33	40.2	8.0	520	10	AV955395	AV955395 AV955395
c	34	39.4	7.9	571	10	AV862022	AV862022 AV862022
	35	39.4	7.9	694	13	BI820797	BI820797 603034004
	36	39.4	7.9	758	13	BI821177	BI821177 603035076
	37	39.4	7.9	824	13	BI911609	BI911609 603064228
	38	39.4	7.9	916	14	BM808544	BM808544 AGENCOURT
	39	39.4	7.9	986	13	BI821324	BI821324 603038167
	40	39.4	7.9	1078	13	BM548310	BM548310 AGENCOURT
	41	39.4	7.9	1129	14	BM807409	BM807409 AGENCOURT
	42	39.4	7.9	1301	13	BM548343	BM548343 AGENCOURT
	43	39.4	7.9	2065	11	BC029282	BC029282 Homo sapi
	44	38.6	7.7	541	14	BM962914	BM962914 cihA9N1T
	45	38.6	7.7	564	10	AV975288	AV975288 AV975288

ALIGNMENTS

RESULT 1
AL698654
LOCUS AL698654 547 bp mRNA linear EST 21-MAR-2002
DEFINITION DKFZp686N12109_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686N12109 5', mRNA sequence.
ACCESSION AL698654
VERSION AL698654.1 GI:19619194
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Duesterhoeft A
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686N12109) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

```
FEATURES             Location/Qualifiers
     source          1. .547
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686N12109"
                     /clone_lib="686 (synonym: hlcc3)"
                     /tissue_type="human skeletal muscle"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
BASE COUNT      112 a    154 c    157 g    124 t
ORIGIN

  Query Match             97.2%;  Score 485.8;  DB 9;  Length 547;
  Best Local Similarity   99.4%;  Pred. No. 7.4e-123;
  Matches  498;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 83

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTG-TTTTTTCCCC 119
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      84 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTTCCCC 143

Qy     120 GGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAA 179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     144 GGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAA 203

Qy     180 CACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCG 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     204 CACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCG 263

Qy     240 CTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGT 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     264 CTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGT 323

Qy     300 TGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 TGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGT 383

Qy     360 CAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGG 419
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 CAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGG 443

Qy     420 CTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCT 479
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Db     444 CTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCT 503

Qy     480 GCAGGAACACTTCCTTGGGTT 500
          |||||||||||||||||||||
Db     504 GCAGGAACACTTCCTTGGGTT 524


RESULT 2
AU135588
LOCUS       AU135588                736 bp    mRNA    linear   EST 02-AUG-2002
DEFINITION  AU135588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
            sequence.
ACCESSION   AU135588
VERSION     AU135588.1  GI:10996127
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
  COMMENT     Contact: Takao Isogai
              Genomics Laboratory
              Helix Research Institute
              1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
              Tel: 81-438-52-3975
              Fax: 81-438-52-3986
              Email: genomics@hri.co.jp
              HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
              Research Institute; cDNA library construction: Department of
              Virology, Institute of Medical Science, University of Tokyo, and
              Helix Research Institute.
  FEATURES             Location/Qualifiers
       source          1. .736
                       /organism="Homo sapiens"
                       /db_xref="taxon:9606"
                       /clone="PLACE1002437"
                       /clone_lib="PLACE1"
                       /tissue_type="placenta"
                       /note="Vector: pME18SFL3"
  BASE COUNT      163 a    199 c    199 g    170 t      5 others
  ORIGIN

    Query Match             96.3%;  Score 481.6;  DB 9;  Length 736;
    Best Local Similarity   99.0%;  Pred. No. 1e-121;
    Matches  495;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

  Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db      25 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 84

  Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db      85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 144

  Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db     145 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 204

  Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
  Db     205 ACAAAAGTGGAAAACAGTTAATGACCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 263

  Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
  Db     264 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTGCTGGCTGAGGGAACATGGCTTGTT 323

  Qy     301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
            |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db     324 GGCCCCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 383

  Qy     361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
            ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db     384 AGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443

  Qy     421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
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  Db     444 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503

  Qy     481 CAGGAACACTTCCTTGGGTT 500
            ||||||||||||||||||||
  Db     504 CAGGAACACTTCCTTGGGTT 523


RESULT 3
Z44377
LOCUS       Z44377                  292 bp    mRNA    linear   EST 14-NOV-1994
DEFINITION  HSC1ZB081 normalized infant brain cDNA Homo sapiens cDNA clone
            c-1zb08, mRNA sequence.
ACCESSION   Z44377
VERSION     Z44377.1  GI:573506
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 292)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
            ,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
            Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1zb08
            Seq primer: (-21)M13_universal.
FEATURES             Location/Qualifiers
     source          1. .292
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="c-1zb08"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total brain
                     ;  total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the  HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,  Psychiatry
                     Dept. Columbia University, USA.  Normalization_method:
                     Bento Soares, P.N.A.S in press"
BASE COUNT       50 a     87 c     96 g     56 t      3 others
ORIGIN

  Query Match            53.7%;  Score 268.4;  DB 14;  Length 292;
  Best Local Similarity  98.2%;  Pred. No. 4.2e-63;
  Matches  280;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 68

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 128

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     129 GTTCTGTTTTCTCCCCTTNTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 188

Qy     181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
             |||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
Db     189 ACAAAAGTGGAAAACAGTTAATGANCAGCCAC-GGCGTCCCTGCTGTGAGCTCTGGCCGC 247

Qy     241 TGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCTGGCTGAG 285
             |||||||||||| |||||||||||||||||| ||||||||||||
Db     248 TGCCTTCCAGGGNTCCCGAGCCACACGCTGGGGGTGCTGGCTGAG 292


RESULT 4
BB657864
LOCUS       BB657864                 619 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB657864 RIKEN full-length enriched, 12 days embryo eyeball Mus
            musculus cDNA clone D230019D04 5', mRNA sequence.
ACCESSION   BB657864
VERSION     BB657864.1  GI:16491690
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="D230019D04"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     eyeball"
                     /tissue_type="eyeball"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
```

```
                 pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT      126 a    185 c    173 g    134 t      1 others
ORIGIN

  Query Match            53.0%;  Score 264.8;  DB 10;  Length 619;
  Best Local Similarity  75.6%;  Pred. No. 3.7e-62;
  Matches  384;  Conservative    0;  Mismatches  112;  Indels   12;  Gaps    4;

Qy          1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
Db         26 GGCCGGGACCGGCAGAGCCCACTTCTCTCCGCGGCGCAGCGC-AAAGCTGGGCAGGGGGC 84

Qy         61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
Db         85 GCCGCGGGACCCGCGCAACCACAGCCGGCTTGGGGAGCTGCTCTGCTCCCTGTTTCCCCC 144

Qy        121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
Db        145 CACTTTTTTCTTCCCCTTTCTGGAAGGGTTTGTGCAGGGGTAGGGAAAACAGACTCAAAC 204

Qy        181 ACAAAAGTGGAAAACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGC 240
Db        205 AGCAAAGTGGAAAACAGTTAATGACCAGCCAC-AGAGTCACAGCTCTGTGCTCTGGCTGC 263

Qy        241 TGCCTTCCAGGGCTCCCGAGCCACA---------CGCTGGGCGTGCTGGCTGAGGGAACA 291
Db        264 T-CCCTCCAGGGCTCTCGAGCCGCAGACGCAGGTCGCTGTGGGTGCCGGCTGTGGTGACA 322

Qy        292 TGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGAC 351
Db        323 TGGCTTGTTGGCCTCAGTTAAGGCTGCTGCTGTGGAAGAATCTGACATTTCGAAGGAGAC 382

Qy        352 AAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCT 411
Db        383 AAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTCTTTATCTTCCTGATCCTGATCT 442

Qy        412 CTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCA 471
Db        443 CTGTACGCCTGAGCTACCCACCCTACGAACAACATGAGTGCCACTTTCCGAATAAAGCCA 502

Qy        472 TGCCCTCTGCAGGAACACTTCCTTGGGT 499
Db        503 TGCCGTCTGCAGGAACCCTCCCCTGGGT 530

RESULT 5
BG384217
LOCUS       BG384217              535 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BG384217
VERSION     BG384217.1  GI:13308689
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 90  row: G  column: 13
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..535
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT      121 a    159 c    136 g    119 t
ORIGIN

  Query Match            51.0%;  Score 254.8;  DB 12;  Length 535;
  Best Local Similarity  76.8%;  Pred. No. 2.1e-59;
  Matches  384;  Conservative    0;  Mismatches   92;  Indels   24;  Gaps    5;

Qy         13 CAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGGGAGCTCCGCGC 72
Db          6 CGGGGCCTTGAGGACACCTCTCTCCCCTGGCGAAGGTGGGCTGGACAGGGGTCTCCGCGC 65

Qy         73 ACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTCCCCGGTTCTGTTTTCT 132
Db         66 TACCAGCGCCGC------CACAGCCAATTTCTCCAGGCACTTT----GCTCCTCTTCCCA 115

Qy        133 CCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAACACAAAAGTGGAA 192
Db        116 CACTTCTCGGGAAGGATTTTTCAAGGGGCAGGGGCAAGAGACGCAAACACAAAAGTGGAA 175

Qy        193 AACAGTTAATGACCAGCCACGGGCGTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGG 252
Db        176 AACAGTTAATGACCAGCCACAG--CGCCCCTGCTTGAGCTCTGGCCACTTCCTCCACGGG 233

Qy        253 CTCCC------GAGCCACACGCTG------GGCGTGCTGGCTGAGGGAACATGGCTTGTT 300
Db        234 GCTCCCGAGCGGAGCCACACGCAGGCTGGTGTGGTGCCAGCTGAGGTAACATGGCTTATT 293

Qy        301 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 360
Db        294 GGACTCAACTGAGGTTACTGCTGTGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTC 353

Qy        361 AGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGC 420
Db        354 AGCTGTTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTGCGGC 413

Qy        421 TGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db        414 TGAGCTACCCACCCTATGAACAACATGAATGTCACTTTCCAAACAAAGCCATGCCCTCTG 473

Qy        481 CAGGAACACTTCCTTGGGTT 500
Db        474 CAGGAACACTTCCTTGGGTT 493

RESULT 6
AU121731
LOCUS       AU121731              763 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU121731 MAMMA1 Homo sapiens cDNA clone MAMMA1000851 5', mRNA
            sequence.
ACCESSION   AU121731
VERSION     AU121731.1  GI:10936966
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
```

```
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MAMMA1000851"
                     /clone_lib="MAMMA1"
                     /tissue_type="mammary gland"
                     /note="Vector: pME18SFL3"
BASE COUNT      137 a    205 c    260 g    158 t      3 others
ORIGIN

  Query Match             39.9%;  Score 199.4;  DB 9;  Length 763;
  Best Local Similarity   99.5%;  Pred. No. 3.4e-44;
  Matches  200;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 82

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      83 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 142

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 202

Qy     181 ACAAAAGTGGAAAACAGTTAA 201
          |||||||||||||||| |||
Db     203 ACAAAAGTGGAAAACAGGTAA 223


RESULT 7
BC034824
LOCUS       BC034824               1004 bp    mRNA    linear   HTC 26-JUL-2002
DEFINITION  Homo sapiens, clone IMAGE:4749735, mRNA.
ACCESSION   BC034824
VERSION     BC034824.1  GI:21961568
KEYWORDS    HTC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1004)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 52 Row: d Column: 19
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 5915657
            This clone has the following problem: incomplete processing.
FEATURES             Location/Qualifiers
     source          1. .1004
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4749735"
                     /tissue_type="Skin, squamous cell carcinoma"
                     /clone_lib="NCI_CGAP_Skn4"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6.ccdb"
BASE COUNT      306 a    234 c    230 g    234 t
ORIGIN

  Query Match             39.6%;  Score 198;  DB 11;  Length 1004;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-44;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 68

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 128

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 188

Qy     181 ACAAAAGTGGAAAACAGT 198
          ||||||||||||||||||
Db     189 ACAAAAGTGGAAAACAGT 206


RESULT 8
BG678861
LOCUS       BG678861               998 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602624760F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5',
            mRNA sequence.
ACCESSION   BG678861
VERSION     BG678861.1  GI:13910258
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 998)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10603  row: g  column: 16
            High quality sequence stop: 860.
FEATURES             Location/Qualifiers
```

```
     source          1. .998
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4749735"
                     /clone_lib="NCI_CGAP_Skn4"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      285 a    233 c    244 g    236 t
ORIGIN

  Query Match             35.6%;  Score 178;  DB 12;  Length 998;
  Best Local Similarity   97.0%;  Pred. No. 2.5e-38;
  Matches  192;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy       1 GGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 60
           ||   ||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GGGGCGGGACCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGG 66

Qy      61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTTGCTCCTTGTTTTTTCCCCG 120
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      67 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGGCGC-TTGCTCCTTGTTTTTTCCCCG 125

Qy     121 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 GTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAC 185

Qy     181 ACAAAAGTGGAAAACAGT 198
           ||||||||||||||||||
Db     186 ACAAAAGTGGAAAACAGT 203


RESULT 9
BI541694
LOCUS       BI541694                 575 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  455529 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI541694
VERSION     BI541694.1  GI:15382806
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 575)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 121  row: M  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .575
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT      102 a    192 c    147 g    134 t
ORIGIN

  Query Match             20.0%;  Score 100;  DB 13;  Length 575;
  Best Local Similarity   67.0%;  Pred. No. 7.1e-17;
  Matches  142;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     288 AACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGA 347
           | |||||| |  ||| | ||||||| | ||||||| |||||||| ||   |   | ||
Db      70 ACCATGGCCTTCTGGACACAGCTGATGCTGCTGCTTTGGAAGAATTTCCTATATCGCAGG 129

Qy     348 AGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTG 407
           || ||  |    || || ||  |||| ||   ||||| || ||| ||||| | ||||||
Db     130 AGGCAGCCGATCCAACTCTTGGTGGAGTTGTTGTGGCCGCTCTTTCTCTTCTTCATCCTG 189

Qy     408 ATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAA 467
           | | ||||| |    | |||| ||    || || |||||||| |||||||| || ||
Db     190 GTGGCCGTTCGCCATTCCCACCCCCACTCGAGCAGCATGAATGTCATTTTCCCAACAAG 249

Qy     468 GCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
           |  ||||||| ||||| ||  | ||||||
Db     250 CCGCTGCCCTCAGCAGGCACCATCCCTTGGCT 281


RESULT 10
AW313960
LOCUS       AW313960                 335 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  9668 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW313960
VERSION     AW313960.1  GI:6743216
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 335)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 8  row: F  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .335
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
```

endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 61 a 107 c 84 g 83 t
ORIGIN

Query Match 18.4%; Score 92; DB 10; Length 335;
Best Local Similarity 64.6%; Pred. No. 1.2e-14;
Matches 137; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

```
Qy    288 AACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGA 347
Db    122 ACCATGGCCTTCTGGACACAGCTAATGCTGCTGCTTTGGAAGAATTTCCTGTATCGCAGG 181

Qy    348 AGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTG 407
Db    182 AGACAGCCGATCCAGCTCTTGGTGGAGTTGATGTGGCCTCTCTTTCTCTTCTTCATTCTG 241

Qy    408 ATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAA 467
Db    242 GTGGCGGTCCGCCATTCCCACCCCCCACTCGAGCAGCATGAATGCCACTTCTCCAACAAG 301

Qy    468 GCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
Db    302 CCGCTTCCTTCAGCCGGTACCATCCCTTGGCT 333
```

RESULT 11
BH042929
LOCUS BH042929 470 bp DNA linear GSS 17-JUL-2001
DEFINITION RPCI-24-285D18.TV RPCI-24 Mus musculus genomic clone RPCI-24-285D18 , DNA sequence.
ACCESSION BH042929
VERSION BH042929.1 GI:14824511
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 470)
AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-24-285D18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 285 row: D column: 18
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .470
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-285D18"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 118 a 95 c 123 g 134 t
ORIGIN

Query Match 17.7%; Score 88.6; DB 17; Length 470;
Best Local Similarity 91.3%; Pred. No. 9.8e-14;
Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy    357 TGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTT 416
Db    308 TGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTCTTTATCTTCCTGATCCTGATCTCTGTA 367

Qy    417 CGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTC 459
Db    368 CGCCTGAGCTACCCACCCTACGAACAACATGAGTGTGAGTATC 410
```

RESULT 12
BM691885
LOCUS BM691885 370 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CL1-aeq-b-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone UI-E-CL1-aeq-b-11-0-UI 5', mRNA sequence.
ACCESSION BM691885
VERSION BM691885.1 GI:19005143
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 370)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 373-413, >POLY_A#Simple_repeat
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .370
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CL1-aeq-b-11-0-UI"
/clone_lib="UI-E-CL1"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CL1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual

```
                    System, supported by National Eye Institute (NEI)."
BASE COUNT      113 a      87 c      83 g      87 t
ORIGIN

  Query Match             17.4%;  Score 87.2;  DB 14;  Length 370;
  Best Local Similarity   60.6%;  Pred. No. 2.4e-13;
  Matches  143;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy     264 CACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTG 323
           ||  |||| | |  ||        | |||||  |    |  ||| |   | |  ||||
Db      23 CAATCTGGTCTTCGTGTGGTCATTAGCATGGGCTTCGTGAGACAGATACAGCTTTTGCTC 82

Qy     324 TGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGG 383
           |||||||||   ||  |  | | ||| ||||    ||   |  |  ||||| | |  |||
Db      83 TGGAAGAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGG 142

Qy     384 CCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAA 443
           ||| ||| | | || ||| || ||||||   |  ||     | |||| | |||    ||
Db     143 CCTTTATCTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCGCTCTACAGCCAT 202

Qy     444 CATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
           |||||||||||||| || || || || |||||||| |||||||  || || ||| |
Db     203 CATGAATGCCATTTCCCCAACAAGGCGATGCCCTCAGCAGGAATGCTGCCGTGGCT 258


RESULT 13
AL712499
LOCUS       AL712499                522 bp    mRNA    linear   EST 22-MAR-2002
DEFINITION  DKFZp686H1289_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686H1289 5', mRNA sequence.
ACCESSION   AL712499
VERSION     AL712499.1  GI:19695855
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            No s1 sequence available.
            This clone (DKFZp686H1289) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .522
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                     /db_xref="taxon:9606"
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                     /clone_lib="686 (synonym: hlcc3)"
                     /tissue_type="human skeletal muscle"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
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  Best Local Similarity   60.6%;  Pred. No. 2.3e-13;
  Matches  143;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy     264 CACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTG 323
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Db     121 TGGAAGAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGG 180

Qy     384 CCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAA 443
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Db     181 CCTTTATCTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCGCTCTACAGCCAT 240

Qy     444 CATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
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Db     241 CATGAATGCCATTTCCCCAACAAGGCGATGCCCTCAGCAGGAATGCTGCCGTGGCT 296


RESULT 14
AL712388
LOCUS       AL712388                523 bp    mRNA    linear   EST 22-MAR-2002
DEFINITION  DKFZp686L0588_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686L0588 5', mRNA sequence.
ACCESSION   AL712388
VERSION     AL712388.1  GI:19695743
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Wambutt R
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686L0588) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
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                     cDNA-collection"
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ORIGIN

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  Best Local Similarity   60.6%;  Pred. No. 2.3e-13;
  Matches  143;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy     264 CACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTG 323
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Db      80 TGGAAGAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGG 139

Qy     384 CCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAA 443
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Db     140 CCTTTATCTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCGCTCTACAGCCAT 199
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Qy    444 CATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
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Db    200 CATGAATGCCATTTCCCCAACAAGGCGATGCCCTCGGCAGGAATGCTGCCGTGGCT 255


RESULT 15
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LOCUS       AL712461                562 bp    mRNA    linear   EST 22-MAR-2002
DEFINITION  DKFZp686D1889_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686D1889 5', mRNA sequence.
ACCESSION   AL712461
VERSION     AL712461.1  GI:19695817
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            No sl sequence available.
            This clone (DKFZp686D1889) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /clone_lib="686 (synonym: hlcc3)"
                     /tissue_type="human skeletal muscle"
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                     cDNA-collection"
BASE COUNT      141 a    139 c    140 g    142 t
ORIGIN

  Query Match           17.4%;  Score 87.2;  DB 9;  Length 562;
  Best Local Similarity   60.6%;  Pred. No. 2.3e-13;
  Matches  143;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy    264 CACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTG 323
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Qy    324 TGGAAGAACCTCACTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGG 383
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Db    114 TGGAAGAACTGGACCCTGCGGAAAAGGCAAAAGATTCGCTTTGTGGTGGAACTCGTGTGG 173

Qy    384 CCTCTATTTATCTTCCTGATCCTGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAA 443
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Db    174 CCTTTATCTTTATTTCTGGTCTTGATCTGGTTAAGGAATGCCAACCCGCTCTACAGCCAT 233

Qy    444 CATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGT 499
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Db    234 CATGAATGCCATTTCCCCAACAAGGCGATGCCCTCAGCAGGAATGCTGCCGTGGCT 289


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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	501	100.0	10442	6	AX060892	AX060892 Sequence
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4	501	100.0	10474	6	AX060719	AX060719 Sequence
5	501	100.0	10474	6	AX060721	AX060721 Sequence
6	501	100.0	10474	6	AX060898	AX060898 Sequence
7	501	100.0	10474	6	AX060900	AX060900 Sequence
8	499.4	99.7	6786	9	AB055982	AB055982 Homo sapi
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13	499.4	99.7	9495	6	AX059978	AX059978 Sequence
14	499.4	99.7	9497	6	AX059973	AX059973 Sequence
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17	499.4	99.7	9741	6	AX127830	AX127830 Sequence
18	499.4	99.7	9741	6	AX139817	AX139817 Sequence
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21	499.4	99.7	9854	6	AX139818	AX139818 Sequence
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24	343.8	68.6	7074	5	AF362377	AF362377 Gallus ga
25	225	44.9	6027	9	AB055390	AB055390 Homo sapi
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27	225	44.9	6704	9	AF328787	AF328787 Homo sapi
28	225	44.9	7795	6	AX429481	AX429481 Sequence
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38	223.4	44.6	6768	6	AX320362	AX320362 Sequence
39	222	44.3	222	6	AX059901	AX059901 Sequence
40	220.4	44.0	222	6	AX127840	AX127840 Sequence
41	220.4	44.0	222	6	AX139827	AX139827 Sequence
42	220.2	44.0	5669	6	AX202220	AX202220 Sequence
43	220.2	44.0	6522	6	AX202218	AX202218 Sequence
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45	217.4	43.4	6607	6	AX080493	AX080493 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX060713 10442 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078972.
ACCESSION AX060713
VERSION AX060713.1 GI:12406103
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;

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           CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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Db    2730 GTGGAGGAAGATGGCTTCAAT 2750


RESULT 2
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LOCUS       AX060892               10442 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078971.
ACCESSION   AX060892
VERSION     AX060892.1  GI:12406270
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 1 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
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ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 10442;
  Best Local Similarity  100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db    2550 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2609

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2610 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2669

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2670 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2729

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2730 GTGGAGGAAGATGGCTTCAAT 2750


RESULT 3
AF285167
LOCUS       AF285167               10442 bp    mRNA    linear   PRI 09-AUG-2000
DEFINITION  Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
            complete cds.
ACCESSION   AF285167
VERSION     AF285167.1  GI:9755158
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Schwartz,K., Lawn,R.M. and Wade,D.P.
  TITLE     ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
            regulated by LXR
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
            Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
            3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES             Location/Qualifiers
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BASE COUNT      2898 a    2297 c    2408 g    2835 t       4 others
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  Query Match             100.0%;  Score 501;  DB 9;  Length 10442;
  Best Local Similarity   100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2310 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2369

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db    2370 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2429

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db    2430 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2489

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db    2490 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2549

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2610 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2669

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2670 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2729

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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Db    2730 GTGGAGGAAGATGGCTTCAAT 2750


RESULT 4
AX060719
LOCUS       AX060719               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078972.
ACCESSION   AX060719
VERSION     AX060719.1  GI:12406108
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 7 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2906 a    2305 c    2416 g    2843 t       4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db    2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db    2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db    2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db    2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db    2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db     2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy      481 GTGGAGGAAGATGGCTTCAAT 501
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Db     2762 GTGGAGGAAGATGGCTTCAAT 2782

RESULT 5
AX060721
LOCUS       AX060721               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 9 from Patent WO0078972.
ACCESSION   AX060721
VERSION     AX060721.1  GI:12406109
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1..10474
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BASE COUNT     2907 a   2304 c   2415 g   2844 t      4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db     2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy      121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db     2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy      181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db     2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy      241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db     2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

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Db     2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy      361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db     2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy      421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db     2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy      481 GTGGAGGAAGATGGCTTCAAT 501
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Db     2762 GTGGAGGAAGATGGCTTCAAT 2782

RESULT 6
AX060898
LOCUS       AX060898               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078971.
ACCESSION   AX060898
VERSION     AX060898.1  GI:12406275
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 7 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1..10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2906 a   2305 c   2416 g   2843 t      4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Qy      121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db     2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy      181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db     2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy      241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db     2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

Qy      301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db     2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy      361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Qy      421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db     2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy      481 GTGGAGGAAGATGGCTTCAAT 501
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Db     2762 GTGGAGGAAGATGGCTTCAAT 2782

RESULT 7
AX060900
LOCUS       AX060900               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 9 from Patent WO0078971.
ACCESSION   AX060900
VERSION     AX060900.1  GI:12406276
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
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BASE COUNT     2907 a    2304 c    2415 g    2844 t      4 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity  100.0%;  Pred. No. 1e-119;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db    2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db    2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db    2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db    2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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Db    2762 GTGGAGGAAGATGGCTTCAAT 2782


RESULT 8
AB055982
LOCUS       AB055982               6786 bp    mRNA    linear   PRI 18-AUG-2001
DEFINITION  Homo sapiens mRNA for ABCA1, complete cds.
ACCESSION   AB055982
VERSION     AB055982.1  GI:15212106
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tanaka,A.R., Abe-Dohmae,S., Arakawa,R., Sadanami,K., Kidera,A.,
            Kioka,N., Amachi,T., Yokoyama,S. and Ueda,K.
  TITLE     A new topological model of functional human ABCA1-Signal peptide
            cleavage and glycosylation of a large extracellular domain
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6786)
  AUTHORS   Ueda,K., Kioka,N. and Tanaka,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate
            School, Applied Life Sciences; Kitashirakawa, Kyoto Sakyo-ku, Kyoto
            606-8502, Japan (E-mail:uedak@kais.kyoto-u.ac.jp,
            Tel:81-75-753-6105, Fax:81-75-753-6104)
FEATURES             Location/Qualifiers
     source          1. .6786
                     /organism="Homo sapiens"
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  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db    2020 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2079

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RESULT 9
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LOCUS       AX253450               6880 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 1 from Patent WO0170810.
ACCESSION   AX253450
VERSION     AX253450.1  GI:16073978
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6880)
  AUTHORS   Schmitz,G. and Bodzioch,M.
  TITLE     Atp binding cassette transporter 1 (abc1) gene polymorphisms and
            uses thereof for the diagnosis and treatment of lipid,
            cardiovascular or inflammatory disorders
  JOURNAL   Patent: WO 0170810-A 1 27-SEP-2001;
            Bayer Aktiengesellschaft (DE)
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ORIGIN

  Query Match           99.7%;  Score 499.4;  DB 6;  Length 6880;
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  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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DEFINITION  Homo sapiens mRNA for ATP-binding cassette transporter-1 (ABC-1).
ACCESSION   AJ012376
VERSION     AJ012376.1  GI:4128032
KEYWORDS    ABC-1 gene; ATP-binding cassette transporter-1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F.,
            Chimini,G., Kaminski,W.E. and Schmitz,G.
  TITLE     Molecular cloning of the human ATP-binding cassette transporter 1
            (hABC1): evidence for sterol-dependent regulation in macrophages
  JOURNAL   Biochem. Biophys. Res. Commun. 257 (1), 29-33 (1999)
  MEDLINE   99194549
   PUBMED   10092505
REFERENCE   2
  AUTHORS   Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F.,
            Chimini,G., Kaminski,W. and Schmitz,G.
  TITLE     Molecular Cloning of the Human ATP-Binding Cassette Transporter 1
            (hABC1): Evidence for Dterol-Dependent Regulation in Macrophages
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97, 7987-7992 (2000)
REFERENCE   3  (bases 1 to 6880)
  AUTHORS   Langmann,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Langmann T., Institute for Clinical
            Chemistry and Laboratory Medicine, University of Regensburg,
            Franz-Josef-Strauss-Allee 11, 93053, GERMANY
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BASE COUNT 1760 a 1656 c 1783 g 1681 t
ORIGIN

Query Match 99.7%; Score 499.4; DB 9; Length 6880;
Best Local Similarity 99.8%; Pred. No. 2.6e-119;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    2020 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2079

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Db    2260 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2319

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2320 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2379

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RESULT 11
AX253452
LOCUS AX253452 7260 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 3 from Patent WO0170810.
ACCESSION AX253452
VERSION AX253452.1 GI:16073979
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7260)
AUTHORS Schmitz,G. and Bodzioch,M.
TITLE Atp binding cassette transporter 1 (abc1) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders
JOURNAL Patent: WO 0170810-A 3 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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BASE COUNT 1834 a 1765 c 1905 g 1756 t
ORIGIN

Query Match 99.7%; Score 499.4; DB 6; Length 7260;
Best Local Similarity 99.8%; Pred. No. 2.6e-119;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    2760 GTGGAGGAAGATGGCTTCAAT 2780
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RESULT 12
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LOCUS       AX092594               7860 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 6 from Patent WO0115676.
ACCESSION   AX092594
VERSION     AX092594.1  GI:13444651
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7860)
  AUTHORS   Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
  TITLE     Compositions and methods for modulating hdl cholesterol and
            triglyceride levels
  JOURNAL   Patent: WO 0115676-A 6 08-MAR-2001;
            University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .7860
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  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db    2154 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2213

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2454 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2513

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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RESULT 13
AX059978
LOCUS       AX059978               9495 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 96 from Patent WO0078970.
ACCESSION   AX059978
VERSION     AX059978.1  GI:12405636
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9495)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 96 28-DEC-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9495
                     /organism="Homo sapiens"
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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RESULT 14
AX059973
LOCUS       AX059973               9497 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 91 from Patent WO0078970.
ACCESSION   AX059973
VERSION     AX059973.1  GI:12405631
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
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          Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
          and Brewer,H.B.
  TITLE   Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL Patent: WO 0078970-A 91 28-DEC-2000;
          Aventis Pharma S.A. (FR)
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Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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RESULT 15
AF165281
LOCUS       AF165281               9497 bp    mRNA    linear   PRI 17-AUG-1999
DEFINITION  Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA,
            complete cds.
ACCESSION   AF165281
VERSION     AF165281.1  GI:5734100
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Tangier disease is caused by mutations in the gene encoding
            ATP-binding cassette transporter 1
  JOURNAL   Nat. Genet. 22 (4), 352-355 (1999)
  MEDLINE   99364413
   PUBMED   10431238
REFERENCE   2  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
            Cr#mieux, Evry 91006, France
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BASE COUNT     2600 a   2115 c   2217 g   2564 t      1 others
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  Best Local Similarity   99.8%;  Pred. No. 2.6e-119;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Searched: 2185239 seqs, 1125999159 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	499.4	99.7	7086	22	ABA09200	Human ABCA1 homolo
11	499.4	99.7	7086	22	AAK52667	Human polynucleoti
12	499.4	99.7	7260	22	AAD21326	Human ATP binding
13	499.4	99.7	7260	22	AAI70315	Human ATP binding
14	499.4	99.7	7281	22	AAK51683	Human polynucleoti
15	499.4	99.7	7857	21	AAC69388	Human ABC1 cholest
16	499.4	99.7	7860	22	AAF83826	Human ABC1 nucleot
17	499.4	99.7	7860	22	AAF92835	Human ABC1 cDNA.
18	499.4	99.7	7864	21	AAC69120	Human ABC1 cholest
19	499.4	99.7	7864	21	AAC69385	Human ABC1 cholest
20	499.4	99.7	7864	21	AAC69386	Human ABC1 cholest
21	499.4	99.7	7864	21	AAC69389	Human ABC1 cholest
22	499.4	99.7	9741	22	AAS06120	Human ABC1 DNA seq
23	499.4	99.7	9741	24	AAD37273	Human ABC1 full-le
24	499.4	99.7	9854	22	AAS06121	Human ABC1 DNA seq
25	483.4	96.5	7861	21	AAC69387	Human ABC1 cholest
26	225	44.9	7795	24	ABL57810	Human ABCA7 coding
27	224	44.7	9181	22	AAS04042	Human ABC1 gene, p
28	224	44.7	20284	21	AAC69139	Human ABC1 gene ex
29	224	44.7	183999	22	AAF92831	Human ABC1 genomic
30	223.4	44.6	6768	24	AAS19207	DNA encoding human
31	223.4	44.6	6791	24	AAL44693	Human transporter
32	220.4	44.0	222	22	AAS06129	Human ABC1 gene po
33	220.2	44.0	5669	22	AAS08707	Human PD-ATP-bindi
34	220.2	44.0	6522	22	AAS08706	Human PD-ATP-bindi
35	217.4	43.4	5762	22	AAF54792	Nucleotide sequenc
36	217.4	43.4	6607	22	AAF54812	Nucleotide sequenc
c 37	205.8	41.1	5811	22	AAD05626	Human secreted pro
38	200.4	40.0	7784	19	AAV33392	ATP binding casset
39	198.8	39.7	7323	21	AAZ94746	Human ATP binding
40	158.6	31.7	5540	24	AAD27271	Human transporter
41	158.6	31.7	7610	24	AAD36299	Human transporter
42	158.6	31.7	8040	22	AAF57452	Human ABCA2 transp
43	158.6	31.7	8195	22	AAH75187	Nucleotide sequenc
44	158.6	31.7	8269	24	ABL53009	Human ATP binding
45	144.2	28.8	6792	22	AAD02722	Human ATP binding

ALIGNMENTS

RESULT 1
AAF24680
ID AAF24680 standard; DNA; 10442 BP.
XX
AC AAF24680;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX

```
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 122-128; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC   membranes and utilises ATP hydrolysis to transport a wide variety of
CC   substrates across the plasma membrane. ABC1 is a pivotal protein in
CC   the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC   stores. ABC1 is defective in Tangier disease, a genetic disorder
CC   characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC   localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC   useful for developing pharmaceutical agents for the treatment of heart
CC   disease and other disorders associated with hypercholesterolemia and
CC   atherosclerosis. The genes are useful for developing screening assays to
CC   screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   are also useful as diagnostic indicators of cardiovascular disease and
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10442;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2250 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2309

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2310 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2369

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db    2370 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2429

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db    2430 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2489

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2490 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2549

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db    2550 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2609

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2610 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2669

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2670 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2729

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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Db    2730 GTGGAGGAAGATGGCTTCAAT 2750

RESULT 2
AAF24702
ID   AAF24702 standard; DNA; 10442 BP.
XX
AC   AAF24702;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of a human ABC1 polypeptide.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             291..7076
FT                   /*tag= a
FT                   /product= "ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31365.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 3; Page 117-123; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC   membranes and utilises ATP hydrolysis to transport a wide variety of
CC   substrates across the plasma membrane. ABC1 is a pivotal protein in
CC   the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC   stores. ABC1 is defective in Tangier disease, a genetic disorder
CC   characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC   localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC   useful for developing pharmaceutical agents for the treatment of heart
CC   disease and other disorders associated with hypercholesterolemia and
CC   atherosclerosis. The genes are useful for developing screening assays to
CC   screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   are also useful as diagnostic indicators of cardiovascular disease and
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10442;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    2250 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2309

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db   2310 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2369

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db   2370 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2429

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Db   2430 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2489

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db   2490 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2549

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2609

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2669

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2729

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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Db   2730 GTGGAGGAAGATGGCTTCAAT 2750
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RESULT 3
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ID   AAF24685 standard; DNA; 10474 BP.
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AC   AAF24685;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag= a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 148-154; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
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  Query Match           100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db   2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db   2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

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Db   2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db   2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db   2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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Db   2762 GTGGAGGAAGATGGCTTCAAT 2782
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ID   AAF24686 standard; DNA; 10474 BP.
XX
AC   AAF24686;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
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XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 170-176; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db    2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db    2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db    2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db    2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

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Db    2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db    2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
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Db    2762 GTGGAGGAAGATGGCTTCAAT 2782


RESULT 5
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ID   AAF24707 standard; DNA; 10474 BP.
XX
AC   AAF24707;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31366.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 27; Page 144-150; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
```

```
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2762 GTGGAGGAAGATGGCTTCAAT 2782


RESULT 6
AAF24708
ID   AAF24708 standard; DNA; 10474 BP.
XX
AC   AAF24708;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag= a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31367.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 30; Page 165-172; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-137;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db    2282 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2341

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2342 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2401

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2402 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2461

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2462 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2521

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2522 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2581
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db    2582 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2641

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2642 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2701

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2702 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2761

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2762 GTGGAGGAAGATGGCTTCAAT 2782
```

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RESULT 7
AAZ94734
ID   AAZ94734 standard; cDNA; 6880 BP.
XX
AC   AAZ94734;
XX
DT   01-AUG-2000  (first entry)
XX
DE   Human ATP binding cassette ABCA1 (ABC1) cDNA.
XX
KW   ABCA1; ABC1; ATP binding cassette; human; cholesterol;
KW   interleukin-1 beta; transporter; inflammation; septic shock;
KW   rheumatoid arthritis; Tangier disease; hypertriglyceridemia;
KW   splenomegaly; atherosclerosis; lipid disorder; dyslipidemia;
KW   psoriasis; lupus erythematosus; diagnosis; gene therapy;
KW   chromosome 9q22-31; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             121..6726
FT                   /*tag=  a
XX
PN   WO200018912-A2.
XX
PD   06-APR-2000.
XX
PF   21-SEP-1999;   99WO-EP06991.
XX
PR   25-SEP-1998;   98US-0101706.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Klucken J;
XX
DR   WPI; 2000-293151/25.
DR   P-PSDB; AAY79380.
XX
PT   Adenosine triphosphate binding proteins useful for identifying agents
PT   for treating atherosclerosis and other inflammatory disorders -
XX
PS   Claim 9; Page 90-93; 154pp; English.
XX
CC   The present sequence is that of human cDNA encoding ATP binding
CC   cassette protein ABCA1 (ABC1, see AAY79380), the human homologue of
CC   mouse ABCA1.  The cDNA was identified using a differential display
CC   method in which monocytes from peripheral blood were subjected to
CC   macrophage differentiation and cholesterol loading with acetylated
CC   low density lipoproteins and subsequent deloading with high density
CC   lipoprotein (HDL3) to identify cholesterol sensitive genes.  The
CC   ABCA1 gene maps to human chromosome 9q22-31.  Dysregulated ABCA1
CC   is the gene locus involved in the HDL deficiency syndrome
CC   Tangier disease, associated with hypertriglyceridemia and
CC   splenomegaly.  ABCA1 is also a transporter for interleukin-1 beta,
CC   making the gene a candidate for treatment of inflammatory diseases
CC   such as rheumatoid arthritis and septic shock.  The invention
CC   also provides other cholesterol-sensitive ABC genes (see AAZ94735-63)
CC   that can be used for diagnostic and therapeutic applications,
CC   and for biochemical or cell-based assays to screen for
CC   pharmacologically active compounds useful for the treatment of
CC   lipid disorders, atherosclerosis or other inflammatory diseases
CC   such as psoriasis and lupus erythematosus.
XX
SQ   Sequence 6880 BP; 1760 A; 1656 C; 1783 G; 1681 T; 0 other;

  Query Match           99.7%;  Score 499.4;  DB 21;  Length 6880;
  Best Local Similarity  99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 1959

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    1960 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2019

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2079

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2139

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2199

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2259

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2319

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2379

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2380 GTGGAGGAAGATGGCTTCAAT 2400
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RESULT 8
AAD21325
ID   AAD21325 standard; cDNA; 6880 BP.
XX
AC   AAD21325;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) cDNA.
XX
KW   Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
KW   dermatological; atherosclerosis; cardiovascular; inflammatory disease;
KW   psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
KW   immunosuppressive; lupus erythematosus; rheumatoid arthritis;
KW   polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             121..6726
FT                   /*tag=  a
FT                   /product= "Human ABC1 protein"
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FT                   /transl_except= (pos:3052-3054, aa:Gln)
FT                   /transl_except= (pos:3058-3060, aa:Lys)
FT   variation       replace (596, A)
FT                   /*tag=  b
FT   variation       replace (1136, C)
FT                   /*tag=  c
FT   variation       replace (2589, G)
FT                   /*tag=  d
FT   variation       replace (3456, C)
FT                   /*tag=  e
XX
PN   EP1136552-A1.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000EP-0105820.
XX
PR   20-MAR-2000; 2000EP-0105820.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640388/74.
DR   P-PSDB; AAE13021.
XX
PT   New adenosine triphosphate binding cassette transporter-1 gene
PT   polymorphisms, useful for diagnosing and treating lipid disorders,
PT   cardiovascular diseases and inflammatory diseases  -
XX
PS   Claim 1; Page 21-23; 48pp; English.
XX
CC   The invention relates to four common polymorphisms in the gene encoding
CC   ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with
CC   decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
CC   ABC1 directly affects cellular lipid homeostasis, which is a key factor
CC   in the atherogenetic processes. The ABC1 polymorphisms are useful for
CC   diagnosing and treating lipid disorders, cardiovascular diseases
CC   (coronary heart disease, atherosclerosis) and inflammatory diseases
CC   (psoriasis, lupus erythematosus). The identification of ABC1 as a
CC   transporter for interleukin-1beta (IL-1beta) identifies this gene as
CC   a candidate for treatment of inflammatory diseases including rheumatoid
CC   arthritis and septic shock. The present sequence is human ABC1 cDNA.
XX
SQ   Sequence 6880 BP; 1760 A; 1658 C; 1781 G; 1681 T; 0 other;

  Query Match             99.7%;  Score 499.4;  DB 22;  Length 6880;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 1959

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    1960 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2019

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2079

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2139

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2199

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2259

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2319

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2379

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2380 GTGGAGGAAGATGGCTTCAAT 2400


RESULT 9
AAI70314
ID   AAI70314 standard; cDNA; 6880 BP.
XX
AC   AAI70314;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) cDNA.
XX
KW   ATP binding cassette transporter 1; ABC1; human; lipid disorder;
KW   cholesterol; cardiovascular disease; inflammatory disease;
KW   antiinflammatory; antilipaemic; antipsoriatic; dermatological;
KW   Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW   polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             121..6726
FT                   /*tag=  a
FT   variation       replace(596,A)
FT                   /*tag=  b
FT   variation       replace(1136,C)
FT                   /*tag=  c
FT   variation       replace(2589,G)
FT                   /*tag=  d
FT   variation       replace(2345,C)
FT                   /*tag=  e
XX
PN   EP1136554-A1.
XX
PD   26-SEP-2001.
XX
PF   24-MAR-2000; 2000EP-0106401.
XX
PR   24-MAR-2000; 2000EP-0106401.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640389/74.
DR   P-PSDB; AAM50227.
XX
PT   New adenosine triphosphate binding cassette transporter gene
PT   polymorphisms, useful for diagnosing and treating lipid disorders,
PT   cardiovascular diseases and inflammatory diseases  -
XX
PS   Claim 1; Page 17-19; 41pp; English.
XX
CC   The present sequence is that of cDNA encoding the human adenosine
CC   triphosphate (ATP) binding cassette transporter 1 (ABC1) protein
CC   (see AAM50227).  The invention provides 4 common polymorphisms in
CC   the ABC1 gene.  These were identified by sequencing the ABC1 gene
CC   in different Tangier kindreds.  In the variant genes, G is changed
CC   to A at position 596 of the present sequence, T is changed to C at
CC   position 1136, A is changed to G at position 2589 or G is changed
CC   to C at position 3456, or any combination of these.  All of these
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CC   polymorphisms alter the amino acid sequence of ABC1 and therefore
CC   may affect its function.  The 2 most common polymorphisms (G596A)
CC   and A2589G) are both associated with a decreased in vitro ApoA-I
CC   mediated efflux of cholesterol from mononuclear phagocytes, a
CC   feature typical of Tangier disease.  3 Of the variants (G596A,
CC   A2589G and G3456C) are significantly increased in a population of
CC   men having low high density lipoprotein-cholesterol levels and
CC   established coronary heart disease (CHD) relative to CHD-free
CC   control subjects.  The use of the provided ABC1 polymorphisms for
CC   the diagnosis and treatment of lipid disorders, cardiovascular
CC   diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC   erythematodes) is claimed.  Modulation of ABC1 transcripts or
CC   proteins by antisense or ribozyme technology or RNA decoys is also
CC   claimed.
XX
SQ   Sequence 6880 BP; 1760 A; 1656 C; 1783 G; 1681 T; 0 other;

  Query Match             99.7%;  Score 499.4;  DB 22;  Length 6880;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 1959

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    1960 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2019

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2079

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2139

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2199

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2259

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2319

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2379

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2380 GTGGAGGAAGATGGCTTCAAT 2400


RESULT 10
ABA09200
ID   ABA09200 standard; cDNA; 7086 BP.
XX
AC   ABA09200;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US03800.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   P-PSDB; ABB11956.
XX
PT   Human proteins and DNA encoding sequences useful for preventing,
PT   treating or ameliorating a medical condition in a mammalian subject
PT   e.g. arthritis and cancer -
XX
PS   Claim 1; Page 833-835; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention.
XX
SQ   Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
```

```
  Query Match             99.7%;  Score 499.4;  DB 22;  Length 7086;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2263 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2322

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2323 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2382

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2442

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2443 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2502

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2562

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2563 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2622

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2623 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2682

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2683 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2742

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2743 GTGGAGGAAGATGGCTTCAAT 2763


RESULT 11
AAK52667
ID   AAK52667 standard; cDNA; 7086 BP.
XX
AC   AAK52667;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 2196.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79534.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 4558-4560; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

  Query Match             99.7%;  Score 499.4;  DB 22;  Length 7086;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2263 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2322

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2323 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2382

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2442

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2443 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2502

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2562

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2563 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2622

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2623 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2682

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2683 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2742

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2743 GTGGAGGAAGATGGCTTCAAT 2763


RESULT 12
```

```
AAD21326
ID   AAD21326 standard; DNA; 7260 BP.
XX
AC   AAD21326;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) gene.
XX
KW   Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;
KW   dermatological; atherosclerosis; cardiovascular; inflammatory disease;
KW   psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
KW   immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..7106
FT                   /*tag= a
FT                   /product= "Human ABC1 protein"
XX
PN   EP1136552-A1.
XX
PD   26-SEP-2001.
XX
PF   20-MAR-2000; 2000EP-0105820.
XX
PR   20-MAR-2000; 2000EP-0105820.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640388/74.
DR   P-PSDB; AAE13022.
XX
PT   New adenosine triphosphate binding cassette transporter-1 gene
PT   polymorphisms, useful for diagnosing and treating lipid disorders,
PT   cardiovascular diseases and inflammatory diseases  -
XX
PS   Example 1; Fig 1; 48pp; English.
XX
CC   The invention relates to four common polymorphisms in the gene encoding
CC   ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with
CC   decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
CC   ABC1 directly affects cellular lipid homeostasis, which is a key factor
CC   in the atherogenetic processes. The ABC1 polymorphisms are useful for
CC   diagnosing and treating lipid disorders, cardiovascular diseases
CC   (coronary heart disease, atherosclerosis) and inflammatory diseases
CC   (psoriasis, lupus erythematosus). The identification of ABC1 as a
CC   transporter for interleukin-1beta (IL-1beta) identifies this gene as
CC   a candidate for treatment of inflammatory diseases including rheumatoid
CC   arthritis and septic shock. The present sequence is human ABC1 gene.
XX
SQ   Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

  Query Match             99.7%;  Score 499.4;  DB 22;  Length 7260;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-136;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2280 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2339

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    2340 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2399

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2400 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2459

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2460 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2519

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2520 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2579

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2580 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2639

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2640 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2699

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2700 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2759

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2760 GTGGAGGAAGATGGCTTCAAT 2780


RESULT 13
AAI70315
ID   AAI70315 standard; cDNA; 7260 BP.
XX
AC   AAI70315;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Human ATP binding cassette transporter 1 (ABC1) cDNA.
XX
KW   ATP binding cassette transporter 1; ABC1; human; lipid disorder;
KW   cholesterol; cardiovascular disease; inflammatory disease;
KW   antiinflammatory; antilipaemic; antipsoriatic; dermatological;
KW   Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW   polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..7106
FT                   /*tag= a
FT   CDS             501..7106
FT                   /*tag= b
FT                   /note= "alternative open reading frame of AAI70314"
FT   variation       replace(976,A)
FT                   /*tag= c
FT   variation       replace(1516,C)
FT                   /*tag= d
FT   variation       replace(2969,G)
FT                   /*tag= e
FT   variation       replace(3836,C)
FT                   /*tag= f
XX
PN   EP1136554-A1.
XX
PD   26-SEP-2001.
XX
PF   24-MAR-2000; 2000EP-0106401.
XX
PR   24-MAR-2000; 2000EP-0106401.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Bodzioch M;
XX
DR   WPI; 2001-640389/74.
DR   P-PSDB; AAM50228.
XX
PT   New adenosine triphosphate binding cassette transporter gene
```

PT polymorphisms, useful for diagnosing and treating lipid disorders,
PT cardiovascular diseases and inflammatory diseases -
XX
PS Disclosure; Page 26-28; 41pp; English.
XX
CC The present sequence is that of cDNA encoding the human adenosine
CC triphosphate (ATP) binding cassette transporter 1 (ABC1) protein
CC (see AAM50227). The sequence includes an extended open reading
CC frame (ORF) to that provided by the sequence in AAI70314, using
CC an alternative ATG codon as initiation codon and thereby adding an
CC extra 40 N-terminal amino acids to the encoded ABC1 protein (see
CC AAM50228). The invention provides 4 common polymorphisms in the
CC ABC1 gene. These were identified by sequencing the ABC1 gene in
CC different Tangier kindreds. In the variant genes (numbering as in
CC AAI70314), G is changed to A at position 596, T is changed to C at
CC position 1136, A is changed to G at position 2589 or G is changed
CC to C at position 3456, or any combination of these. All of these
CC polymorphisms alter the amino acid sequence of ABC1 and therefore
CC may affect its function. The 2 most common polymorphisms (G596A)
CC and A2589G) are both associated with a decreased in vitro ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 Of the variants (G596A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABC1 polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC erythematodes) is claimed. Modulation of ABC1 transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.
XX
SQ Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match 99.7%; Score 499.4; DB 22; Length 7260;
Best Local Similarity 99.8%; Pred. No. 2.1e-136;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2280 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2339

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    2340 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2399

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2400 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2459

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2460 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2519

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2520 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2579

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2580 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2639

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2640 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2699

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2700 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2759

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2760 GTGGAGGAAGATGGCTTCAAT 2780
```

RESULT 14
AAK51683
ID AAK51683 standard; cDNA; 7281 BP.
XX
AC AAK51683;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 228.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM78550.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 1; Page 1086-1096; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;

Query Match 99.7%; Score 499.4; DB 22; Length 7281;
Best Local Similarity 99.8%; Pred. No. 2.1e-136;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db    2301 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2360
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Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db    2361 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2420

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2421 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2480

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db    2601 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2660

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2661 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2720

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2781 GTGGAGGAAGATGGCTTCAAT 2801
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RESULT 15
AAC69388
ID AAC69388 standard; cDNA; 7857 BP.
XX
AC AAC69388;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX
DR WPI; 2000-587528/55.
DR P-PSDB; AAB38107.
XX
PT New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT disease and cancer -
XX
PS Examples; Page -; 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC transporter associated with an altered cholesterol level and therefore an
CC altered risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;

Query Match 99.7%; Score 499.4; DB 21; Length 7857;
Best Local Similarity 99.8%; Pred. No. 2.2e-136;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2456 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2515

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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Db   2516 GTGGAGGAAGATGGCTTCAAT 2536


Search completed: April  3, 2003, 13:36:30
Job time : 114.452 secs
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 Seconds
(without alignments)
11152.306 Million cell updates/sec

Title: US-09-595-526C-1_COPY_2250_2750
Perfect score: 501
Sequence: 1 gtgatcatcaagggcatcgt.....tggaggaagatggcttcaat 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	124.2	24.8	5894	3	US-08-665-259-24	Sequence 24, Appl
	2	124.2	24.8	5894	3	US-08-762-500-24	Sequence 24, Appl
	3	124.2	24.8	6525	3	US-08-762-500-74	Sequence 74, Appl
	4	46	9.2	7218	1	US-08-232-463-14	Sequence 14, Appl
c	5	34.8	6.9	4350	4	US-09-295-593-37	Sequence 37, Appl
	6	33.4	6.7	961	4	US-09-149-476-284	Sequence 284, App
	7	33	6.6	6048	4	US-09-634-920-3	Sequence 3, Appli
	8	32.8	6.5	1021	4	US-09-149-476-145	Sequence 145, App
	9	32.4	6.5	488	4	US-09-280-116-109	Sequence 109, App
c	10	32.4	6.5	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c	11	32	6.4	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	12	31.8	6.3	606	4	US-09-328-111-133	Sequence 133, App
c	13	31.8	6.3	2912	4	US-09-307-143-3	Sequence 3, Appli
c	14	31.8	6.3	3105	4	US-08-542-635-1	Sequence 1, Appli
c	15	31.2	6.2	1494	1	US-08-318-905-21	Sequence 21, Appl
c	16	31.2	6.2	1494	1	US-08-483-232-21	Sequence 21, Appl
c	17	31.2	6.2	1494	1	US-08-483-140-21	Sequence 21, Appl
c	18	31.2	6.2	1494	2	US-08-485-938A-21	Sequence 21, Appl
c	19	31.2	6.2	1494	2	US-08-910-041-21	Sequence 21, Appl
c	20	31.2	6.2	1494	3	US-09-328-474-21	Sequence 21, Appl
c	21	31.2	6.2	1494	3	US-09-100-546-21	Sequence 21, Appl
c	22	31.2	6.2	1494	3	US-09-010-715-21	Sequence 21, Appl
c	23	31.2	6.2	1494	4	US-09-577-758-21	Sequence 21, Appl
	24	30.8	6.1	1089	4	US-09-513-838-1	Sequence 1, Appli
	25	30.8	6.1	1368	4	US-09-227-357-98	Sequence 98, Appl
	26	30.8	6.1	2328	4	US-09-513-838-5	Sequence 5, Appli
	27	30.6	6.1	246240	2	US-08-724-394A-20	Sequence 20, Appl
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	34	30.4	6.1	1683	2	US-08-456-489B-5	Sequence 5, Appli
	35	30.4	6.1	1683	5	PCT-US93-01720-5	Sequence 5, Appli
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	37	30.4	6.1	1947	2	US-08-456-489B-4	Sequence 4, Appli
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	39	30.4	6.1	1997	1	US-08-164-614A-6	Sequence 6, Appli
	40	30.4	6.1	1997	2	US-08-456-489B-6	Sequence 6, Appli
	41	30.4	6.1	1997	5	PCT-US93-01720-6	Sequence 6, Appli
c	42	30.4	6.1	3882	4	US-09-484-970B-68	Sequence 68, Appl
	43	30.2	6.0	1040	4	US-09-183-959-11	Sequence 11, Appl
c	44	29.8	5.9	728	4	US-09-221-017B-10	Sequence 10, Appl
	45	29.8	5.9	4134	4	US-09-162-021B-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
;    APPLICANT:  Klinger, Katherine W.
;    TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;    TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,259
;      FILING DATE:  17-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-9.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 872-8400
;      TELEFAX:  (508) 872-5415
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5894 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..5053
US-08-665-259-24

  Query Match             24.8%;  Score 124.2;  DB 3;  Length 5894;
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  Matches  274;  Conservative    0;  Mismatches  208;  Indels   15;  Gaps    1;

Qy      17 TCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACA 76
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Db     786 TCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACATGCGCATGATGGGGCTCAGCAGCT 845

Qy      77 GCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCC 136
           |  | | ||||  |  ||||||| |     | || |    || ||  |   |||   |
Db     846 GGCTGCACTGGAGTGCCTGGTTCCTCTTGTTCTTCCTCTTCCTCCTCATCGCCGCCTCCT 905

Qy     137 TGCTAGTGGTCATCCTGAAGTTA--------------GGAAACCTGCTGCCCTACAGTG 181
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Db    1146 GCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTCGCCATGGCAATGGGAGCCCAGCTCA 1205

Qy     422 TTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTG 481
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Qy     482 TGGAGGAAGATGGCTTC 498
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Db    1266 ACGTGGACGACGACTTC 1282


RESULT 2
US-08-762-500-24
; Sequence 24, Application US/08762500
; Patent No. 6030806
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
;    APPLICANT:  Klinger, Katherine W.
;    TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;    TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/762,500
;      FILING DATE:  09-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,259
;      FILING DATE:  17-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10469
;      FILING DATE:  17-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-9.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 872-8400
;      TELEFAX:  (508) 872-5415
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5894 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..5053
US-08-762-500-24

  Query Match             24.8%;  Score 124.2;  DB 3;  Length 5894;
  Best Local Similarity   55.1%;  Pred. No. 5e-29;
  Matches  274;  Conservative    0;  Mismatches  208;  Indels   15;  Gaps    1;

Qy      17 TCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACA 76
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Qy      77 GCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCC 136
           |  | | ||||  |  ||||||| |     | || |    || ||  |   |||   |
Db     846 GGCTGCACTGGAGTGCCTGGTTCCTCTTGTTCTTCCTCTTCCTCCTCATCGCCGCCTCCT 905

Qy     137 TGCTAGTGGTCATCCTGAAGTTA--------------GGAAACCTGCTGCCCTACAGTG 181
           |  |     |  || |     |              | |  | ||||| ||  ||| |
Db     906 TCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTGCTGTCCCGCAGCG 965

Qy     182 ATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCT 241
           | |||  | ||||| | | |||||||      || ||  |    || |||       |||
Db     966 ACCCCTCCCTGGTGCTCGCCTTCCTGCTGTGCTTCGCCATCTCTACCATCTCCTTCAGCT 1025

Qy     242 TCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCT 301
           || || | |||||  |||||  || ||||||| ||||||||||||  || ||| || |||
Db    1026 TCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGCAGCAGCCTTCGGAGGCTTCCTCT 1085

Qy     302 ACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCA 361
           |||||      ||| | |||||| || |    |   || |  |||   ||    | |
Db    1086 ACTTCTTCACCTACATCCCCTACTTCTTCGTGGCCCCTCGGTACAACTGGATGACTCTGA 1145

Qy     362 CACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACT 421
           |  ||| ||| | |  |||| ||||||  ||| ||  | |  | ||    || |
Db    1146 GCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTCGCCATGGCAATGGGAGCCCAGCTCA 1205

Qy     422 TTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTG 481
           |||      ||||||| | | |||||  ||  | ||||||    ||||  |
Db    1206 TTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTGGCGAGACCTCCTGAGTCCCGTCA 1265

Qy     482 TGGAGGAAGATGGCTTC 498
           | ||| || | ||||
Db    1266 ACGTGGACGACGACTTC 1282


RESULT 3
US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
```

; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 573..5684
US-08-762-500-74

Query Match 24.8%; Score 124.2; DB 3; Length 6525;
Best Local Similarity 55.1%; Pred. No. 5.3e-29;
Matches 274; Conservative 0; Mismatches 208; Indels 15; Gaps 1;

Qy 17 TCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACA 76
Db 1417 TCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACATGCGCATGATGGGGCTCAGCAGCT 1476

Qy 77 GCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCC 136
Db 1477 GGCTGCACTGGAGTGCCTGGTTCCTCTTGTTCTTCCTCTTCCTCCTCATCGCCGCCTCCT 1536

Qy 137 TGCTAGTGGTCATCCTGAAGTTA----------GGAAACCTGCTGCCCTACAGTG 181
Db 1537 TCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTGCTGTCCCGCAGCG 1596

Qy 182 ATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCT 241
Db 1597 ACCCCTCCCTGGTGCTCGCCTTCCTGCTGTGCTTCGCCATCTCTACCATCTCCTTCAGCT 1656

Qy 242 TCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCT 301
Db 1657 TCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGCAGCAGCCTTCGGAGGCTTCCTCT 1716

Qy 302 ACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCA 361
Db 1717 ACTTCTTCACCTACATCCCCTACTTCTTCGTGGCCCCTCGGTACAACTGGATGACTCTGA 1776

Qy 362 CACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACT 421
Db 1777 GCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTCGCCATGGCAATGGGAGCCCAGCTCA 1836

Qy 422 TTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTG 481
Db 1837 TTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTGGCGAGACCTCCTGAGTCCCGTCA 1896

Qy 482 TGGAGGAAGATGGCTTC 498
Db 1897 ACGTGGACGACGACTTC 1913

RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 9.2%; Score 46; DB 1; Length 7218;
Best Local Similarity 5.6%; Pred. No. 0.00022;
Matches 22; Conservative 206; Mismatches 166; Indels 0; Gaps 0;

Qy 39 GCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTT 98
Db 1017 GCTCACAGAATTAATTCCGAGCTTGGCTGCAGGTCGAGGGAGCTTGCGATYYYYYYYYYY 1076

Qy 99 CATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTT 158
Db 1077 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1136

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Qy     159 AGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGC 218
           ::: :: :::: :  :  ::::  : :  : ::: :::::::: ::: : ::: :
Db    1137 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1196

Qy     219 TGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGC 278
           : :  :  :  :::: :  : :::::  ::  : : :::::::::    ::  :::  :
Db    1197 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1256

Qy     279 AGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGC 338
             :  ::: :     : :: ::: :::: : :: : ::: :::: : :::: : : :  :
Db    1257 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1316

Qy     339 ATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGC 398
           :  :    :: : :  :::: : :::    ::::: ::  ::: :: :::::: :  :
Db    1317 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1376

Qy     399 TTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTT 432
           ::::   :::  :: :   : :::: ::::::::
Db    1377 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1410


RESULT 5
US-09-295-593-37/c
; Sequence 37, Application US/09295593
; Patent No. 6417169
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping H.
;  APPLICANT: LEE, Yoon S.
;  TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
;  TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
;  TITLE OF INVENTION: GROWTH
;  FILE REFERENCE: 032396-046
;  CURRENT APPLICATION NUMBER: US/09/295,593
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: US 60/082,791
;  EARLIER FILING DATE: 1998-04-23
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 4350
;   TYPE: DNA
;   ORGANISM: Human
US-09-295-593-37

  Query Match             6.9%;  Score 34.8;  DB 4;  Length 4350;
  Best Local Similarity   58.8%;  Pred. No. 0.55;
  Matches   60;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     382 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAG 441
           |||   || | ||||  |  || || ||  |||| || || || | || |    | || |
Db    1827 CTGTGTTCGCGTGTGTGTGCTGTGTGTGCATGTGTGTGCTGTGTCTTTGTGTGTGTGCTG 1768

Qy     442 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTG 483
           |   | | |||| ||| |   |  ||| || | || |||||
Db    1767 TGTGCTAGTGTGCTGTGTGTGCATGTGTGTGCGTGTGCTGTG 1726


RESULT 6
US-09-149-476-284
; Sequence 284, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,583
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,617
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,618
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,503
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,592
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,581
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,584
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,587
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,613
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,582
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,596
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,612
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,580
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,568
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,314
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,569
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,311
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,671
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,674
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,669
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
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; EARLIER APPLICATION NUMBER: 60/056,910
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; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.7%; Score 33.4; DB 4; Length 961;
Best Local Similarity 46.6%; Pred. No. 0.68;
Matches 103; Conservative 1; Mismatches 117; Indels 0; Gaps 0;

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Qy    270 CAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCT 329
          ||||||||  ||  ||     ||| | |       | ||  |  |  || |  ||  | | ||
Db    490 CAACCTGGTAGGGGCTCTGCGGGCCCTGGCAGCCATCCTGGAGCGCCGGGCCGCCATGCT 549

Qy    330 GTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTC 389
          | |  ||     || ||    | | | | |    ||    | |||     ||||||  |
Db    550 GCGCCTGTTGCTGCTGGTGGCCTTTGCCCTGGTGGTCGTCCTGTTCCACGTCCTGCTTGC 609

Qy    390 TCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 449
          |||  |  |       ||   |    | | || || |    |  ||||   ||||  | |
Db    610 TCCCATCACAGCCCTCTTCCACACCCACTTCTATGACAGGCTACAGGACGCGGGCTCTCG 669

Qy    450 AGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAG 490
            ||    |  | |||| | :  |||  |||  || | ||
Db    670 CTGGCCCGAGCTCTACCTCTAYTCGAGGGCTGACGAAGTAG 710
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RESULT 7
US-09-634-920-3
; Sequence 3, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME

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;  FILE REFERENCE:  2323-155
;  CURRENT APPLICATION NUMBER: US/09/634,920
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/190,057
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  60/147,488
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6048
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(6048)
US-09-634-920-3

  Query Match             6.6%;  Score 33;  DB 4;  Length 6048;
  Best Local Similarity   53.5%;  Pred. No. 2.4;
  Matches   69;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy     133 GGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTG 192
           | || ||      | ||| | |||   |    ||| |   | ||   | |   | |||
Db    2071 GCCCAGCGCTACCTGATCTGGGAGTGCTGCCCGCTGTGGATGTCCATCAAGCAGGGAGTG 2130

Qy     193 GTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGC 252
           ||| ||  || ||  |  |||| |||   | || |||     |||| || |  | | |
Db    2131 AAGTTGGTGGTCATGGACCCGTTTACTGACCTCACCATCACTATGTGCATCGTACTCAAC 2190

Qy     253 ACACTCTTC 261
           |||||||||
Db    2191 ACACTCTTC 2199


RESULT 8
US-09-149-476-145
; Sequence 145, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,583
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,617
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,618
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,503
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,592
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,581
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,584
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,587
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,613
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,582
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,596
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,612
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,580
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,568
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,314
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,569
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,311
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,671
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,674
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,669
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,312
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,313
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,672
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,315
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/056,886
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,877
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,889
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,893
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,630
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,878
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,662
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.5%; Score 32.8; DB 4; Length 1021;
Best Local Similarity 46.6%; Pred. No. 1.1;
Matches 103; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

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Qy    270 CAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCT 329
          ||||||||  ||  ||     ||| | |       | ||  |  |  || | ||  | | ||
Db    520 CAACCTGGTAGGGGCTCTGCGGGCCCTGGCAGCCATCCTGGAGCGCCGGGCCGCCATGCT 579

Qy    330 GTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTC 389
          | |  ||     || ||    | | | | |     ||    | |||     ||||||  |
Db    580 GCGCCTGTTGCTGCTGGTGGCCTTTGCCCTGGTGGTCGTCCTGTTCCACGTCCTGCTTGC 639

Qy    390 TCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 449
          |||  |  |       ||   |    | | || || |    |  ||||  ||||  | |
Db    640 TCCCATCACAGCCNTCTTCCACACCCACTTCTATGACAGGCTACAGGACGCGGGCTCTCG 699

Qy    450 AGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAG 490
            ||    |  | |||| |   |||  |||  || | ||
Db    700 CTGGCCCGAGCTCTACCTCTACTCGAGGGCTGACGAAGTAG 740
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RESULT 9
US-09-280-116-109
; Sequence 109, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-109

Query Match 6.5%; Score 32.4; DB 4; Length 488;
Best Local Similarity 50.6%; Pred. No. 0.98;
Matches 78; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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Qy    212 TGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCA 271
          || |  ||||||  ||   ||||  |     | |||    | |   || ||   | |||
Db     38 TGCTGACTGTGGCCACCGCCCTGATGCTGCCCGTGAAGCCCCCCGGCTCCTGGGGGGCCC 97

Qy    272 ACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGT 331
          |  |    |  | |   | ||  | |  | ||| || ||  ||| || | | ||| |  |
Db     98 AGATCATCGGGGGCCACGAGGTGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT 157

Qy    332 GTGTGGCATGGCAGGACTACGTGGGCTTCACACT 365
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Db    158 TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCT 191


RESULT 10
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             6.5%;  Score 32.4;  DB 4;  Length 4403765;
  Best Local Similarity   56.6%;  Pred. No. 57;
  Matches   60;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy    344 AGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTG 403
Db 4072293 AGGGCAACGGCCGCTCGACCCGCGAGTTCTTCGATCTCCTGTTGTCCGAACGCGGTTCTG 4072234

Qy    404 GGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 449
Db 4072233 GCCTCGACTGGGGGAAGACCGACCTGGAAGAGTTGCACGGCGCTTG 4072188


RESULT 11
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             6.4%;  Score 32;  DB 4;  Length 4411529;
  Best Local Similarity   56.6%;  Pred. No. 62;
  Matches   60;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy    344 AGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTG 403
Db 4080115 AGGGCAACGGCCGCTCGACCCGCGAGTTCTTCGATCTCCTGTTGTCCGAACGCGGTTCTG 4080056

Qy    404 GGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 449
Db 4080055 GCCTCGACTGGGGGAAGACCGACCTGGAAGAGTTGCACGGCGCTTG 4080010


RESULT 12
US-09-328-111-133
; Sequence 133, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
;   LENGTH: 606
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(606)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-133

  Query Match             6.3%;  Score 31.8;  DB 4;  Length 606;
  Best Local Similarity   49.1%;  Pred. No. 1.7;
  Matches   84;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy    105 TAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAA 164
Db     13 TAATCTTCTTCTTCTTCTTCTTGTCACCATCCTTCTTTTCTTCTTCCTCATCAGAACCAA 72

Qy    165 CCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGT 224
Db     73 CATCTTCAATTTCAGGTTTGTCTTCCGACTCTTTCTCTTCTTTTTCTTTTTCTTCTTCTT 132

Qy    225 GACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCT 275
Db    133 TGTCTTCCTTTTCTTCAGCCTCATCATCGCTTACTTCTTTATCACGTTCCT 183


RESULT 13
US-09-307-143-3/c
; Sequence 3, Application US/09307143
; Patent No. 6335157
; GENERAL INFORMATION:
;  APPLICANT: Gonzalez c.
;  APPLICANT: Lange, B.
;  TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE
;  TITLE OF INVENTION: CENTROSOME
;  FILE REFERENCE: 9882-003
;  CURRENT APPLICATION NUMBER: US/09/307,143
;  CURRENT FILING DATE: 1999-05-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 3
;   LENGTH: 2912
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(2256)
US-09-307-143-3

  Query Match             6.3%;  Score 31.8;  DB 4;  Length 2912;
  Best Local Similarity   49.1%;  Pred. No. 3.9;
  Matches   84;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy     105 TAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAA 164
           ||  ||  ||| |||||||  |   | |   ||| ||  |  || |||| |    |   ||
Db     901 TAATCTTCTTCTTCTTCTTCTTGTCACCATCCTTCTTTTCTTCTTCCTCATCAGAACCAA 842

Qy     165 CCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGT 224
           | |  |    | |||   |  | |    | ||| |||||  | | | | ||     |  |
Db     841 CATCTTCAATTTCAGGTTTGTCTTCCGACTCTTTCTCTTCTTTTTCTTTTTCTTCTTCTT 782

Qy     225 GACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCT 275
               ||||    | |  ||| || | | |   |||||  |   |   |||
Db     781 TGTCTTCCTTTTCTTCAGCCTCATCATCGCTTACTTCTTTATCACGTTCCT 731


RESULT 14
US-08-542-635-1/c
; Sequence 1, Application US/08542635
; Patent No. 6218356
;  GENERAL INFORMATION:
;    APPLICANT:  Pawson, Anthony
;    APPLICANT:  Henkemeyer, Mark
;    APPLICANT:  Letwin, Kenneth
;    TITLE OF INVENTION:  NOVEL NEURAL RECEPTOR
;    TITLE OF INVENTION:  TYROSINE KINASE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bereskin & Parr
;      STREET:  40 King Street West, Box 401
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/542,635
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDiarmid, Shona S.
;      REGISTRATION NUMBER:  38,798
;      REFERENCE/DOCKET NUMBER:  3153-162
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 364-7311
;      TELEFAX:  (416) 361-1398
;      TELEX:  06-23115
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
;      DEVELOPMENTAL STAGE:  Embryo
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda gt10 cDNA library
;      CLONE:  Combined PnUKRACE A2 and K2 AND cDNA clones
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  Distal end of chromosome 4
;      MAP POSITION:  near the ahd-1 mutation
US-08-542-635-1

  Query Match             6.3%;  Score 31.8;  DB 4;  Length 3105;
  Best Local Similarity   48.1%;  Pred. No. 4;
  Matches   90;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy      19 GTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGC 78
           |||   ||| || ||| || |  | | | |  || | |   | |||     ||  | | |
Db    3060 GTGACAGAGCAGCAGGGACCGACGTAGGGGCTCAGGGGCGGCGTGGAGGAAGAGGAGAAC 3001

Qy      79 ATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTG 138
             |  | ||   | |    | |    || ||   ||   |||.| || || |    |
Db    3000 CGAGGCAGGCGAATGTCAAACCTCTACAGACTGGATCTGGTTCATCTGGGCCCGCATCAC 2941

Qy     139 CTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTT 198
           || |      | | | | ||          ||     ||| ||||| |||| || || |  |
Db    2940 CTGGATACTGTTCAGGATTTTTTTCTGGTGGCCAGCTAGAGTGACCCCAACGCGGAGAAT 2881

Qy     199 GTCTTCC 205
           ||| |||
Db    2880 GTCCTCC 2874


RESULT 15
US-08-318-905-21/c
; Sequence 21, Application US/08318905
; Patent No. 5641669
;  GENERAL INFORMATION:
;    APPLICANT:  Cousens, Lawrence S.
;    APPLICANT:  Eberhardt, Christine D.
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Le Trong, Hai
;    APPLICANT:  Tjoelker, Larry W.
;    APPLICANT:  Wilder, Cheryl L.
;    TITLE OF INVENTION:  Platelet-Activating Factor Acetyl
;    TITLE OF INVENTION:  Hydrolase
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gertein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,905
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,803
;      FILING DATE:  6-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5641669and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32205
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3658
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1494 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  117..1436
US-08-318-905-21

  Query Match              6.2%;  Score 31.2;  DB 1;  Length 1494;
  Best Local Similarity   46.4%;  Pred. No. 4.2;
  Matches  102;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

Qy      53 TGCGGATCATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCA 112
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Db    1408 TGCTGAGCCGGGGCCTGGGTGACTGCGTCAAAGGGTGACCCAGGAATCAGGTTCTCATCA 1349

Qy     113 TTCCTCTTCTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGC 172
           |  |  | |    ||| |     ||| |    ||| | ||||||     ||  ||  ||
Db    1348 TCTCCTTCCACCAGAGGGTCCCACTGATCAAAGTCTTTCTGAAGCCCTAAATGCTTTTGT 1289

Qy     173 CCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCC 232
              | ||  |||  ||| | ||   ||  ||     |   | ||   | |       |
Db    1288 AAGAAAGCCATCGAAGCTTTGTTGGTGAGGTCGATGGCTACTCTGGAATCGATTTCTCCT 1229

Qy     233 TGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAA 272
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Db    1228 TTCAGTGTCAGCTTGTTTCCAATTATTTTGCCAGTTACAA 1189


Search completed: April  3, 2003, 14:21:36
Job time : 4321.78 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 31.6923 Seconds
(without alignments)
13866.500 Million cell updates/sec

Title: US-09-595-526C-1_COPY_2250_2750
Perfect score: 501
Sequence: 1 gtgatcatcaagggcatcgt.....tggaggaagatggcttcaat 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	501	100.0	9870	9	US-09-984-827-101	Sequence 101, App
2	499.4	99.7	8925	9	US-09-802-640-27	Sequence 27, Appl
3	499.4	99.7	9741	9	US-09-984-827-1	Sequence 1, Appli
4	499.4	99.7	9741	10	US-09-846-456-10	Sequence 10, Appl
5	499.4	99.7	9870	9	US-09-984-827-92	Sequence 92, Appl
6	499.4	99.7	9870	9	US-09-984-827-93	Sequence 93, Appl
7	499.4	99.7	9870	9	US-09-984-827-94	Sequence 94, Appl
8	499.4	99.7	9870	9	US-09-984-827-95	Sequence 95, Appl
9	499.4	99.7	9870	9	US-09-984-827-96	Sequence 96, Appl
10	499.4	99.7	9870	9	US-09-984-827-97	Sequence 97, Appl
11	499.4	99.7	9870	9	US-09-984-827-98	Sequence 98, Appl
12	499.4	99.7	9870	9	US-09-984-827-99	Sequence 99, Appl
13	499.4	99.7	9870	9	US-09-984-827-100	Sequence 100, App
14	499.4	99.7	9870	9	US-09-984-827-103	Sequence 103, App
15	499.4	99.7	9870	9	US-09-984-827-104	Sequence 104, App
16	499.4	99.7	9870	9	US-09-984-827-105	Sequence 105, App
17	499.4	99.7	9870	9	US-09-984-827-106	Sequence 106, App
18	499.4	99.7	9870	9	US-09-984-827-107	Sequence 107, App
19	499.4	99.7	9870	9	US-09-984-827-108	Sequence 108, App
20	499.4	99.7	9870	9	US-09-984-827-109	Sequence 109, App
21	499.4	99.7	9870	9	US-09-984-827-110	Sequence 110, App
22	499.4	99.7	9870	9	US-09-984-827-111	Sequence 111, App
23	499.4	99.7	9870	9	US-09-984-827-112	Sequence 112, App
24	499.4	99.7	9870	9	US-09-984-827-113	Sequence 113, App
25	499.4	99.7	9870	9	US-09-984-827-114	Sequence 114, App
26	499.4	99.7	9870	9	US-09-984-827-115	Sequence 115, App
27	499.4	99.7	9870	9	US-09-984-827-116	Sequence 116, App
28	499.4	99.7	9870	9	US-09-984-827-117	Sequence 117, App
29	499.4	99.7	9870	9	US-09-984-827-118	Sequence 118, App
30	499.4	99.7	9870	9	US-09-984-827-119	Sequence 119, App
31	499.4	99.7	9870	9	US-09-984-827-120	Sequence 120, App
32	499.4	99.7	9870	9	US-09-984-827-121	Sequence 121, App
33	499.4	99.7	9870	9	US-09-984-827-122	Sequence 122, App
34	499.4	99.7	9870	9	US-09-984-827-123	Sequence 123, App
35	499.4	99.7	9870	9	US-09-984-827-124	Sequence 124, App
36	499.4	99.7	9870	9	US-09-984-827-125	Sequence 125, App
37	499.4	99.7	9870	9	US-09-984-827-126	Sequence 126, App
38	497.8	99.4	9870	9	US-09-984-827-102	Sequence 102, App
39	224	44.7	9181	9	US-09-984-827-10	Sequence 10, Appl
40	223.4	44.6	4653	10	US-09-995-542-7	Sequence 7, Appli
41	223.4	44.6	6432	10	US-09-858-194-3	Sequence 3, Appli
42	223.4	44.6	6768	10	US-09-858-194-1	Sequence 1, Appli
43	223.4	44.6	6804	10	US-09-995-542-4	Sequence 4, Appli
44	220.4	44.0	222	9	US-09-984-827-47	Sequence 47, Appl
45	215.8	43.1	6633	10	US-09-995-542-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-984-827-101
; Sequence 101, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-101

Query Match 100.0%; Score 501; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 1.1e-154;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db   2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db   2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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Db   2753 GTGGAGGAAGATGGCTTCAAT 2773
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RESULT 2
US-09-802-640-27
; Sequence 27, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kleyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 8925
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5020)...(6162)
; OTHER INFORMATION: Nucleotide encoding ATP-binding cassette (ABC1)
; OTHER INFORMATION: n= a or g or c or t
US-09-802-640-27

Query Match 99.7%; Score 499.4; DB 9; Length 8925;
Best Local Similarity 99.8%; Pred. No. 3.6e-154;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   1899 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 1958

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1959 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2018

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2019 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2078

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db   2199 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2258

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Qy    481 GTGGAGGAAGATGGCTTCAAT 501
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RESULT 3
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; Sequence 1, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7009)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-1

Query Match 99.7%; Score 499.4; DB 9; Length 9741;
Best Local Similarity 99.8%; Pred. No. 3.7e-154;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   2144 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2203

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db   2204 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2263

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
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Db   2264 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2323

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db   2324 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2383

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2443

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db   2444 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2503

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2563

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db   2564 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2623

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2624 GTGGAGGAAGATGGCTTCAAT 2644


RESULT 4
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
;  APPLICANT: Rosier, Marie
;  APPLICANT:  Prades, Catherine
;  APPLICANT:  Lemoine, Cendrine
;  APPLICANT:  Naudin, Laurent
;  APPLICANT:  Denefle, Patrice
;  APPLICANT:  Duverger, Nicolas
;  APPLICANT:  Brewer, Bryan
;  APPLICANT:  Remaley, Alan
;  APPLICANT:  Fojo, Silvia
;  TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
;  TITLE OF INVENTION:  Activity and Therapeutic Uses
;  FILE REFERENCE: 3806.0505
;  CURRENT APPLICATION NUMBER: US/09/846,456
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,280
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 9741
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

  Query Match             99.7%;  Score 499.4;  DB 10;  Length 9741;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db   2144 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2203

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db   2204 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2263

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2323

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2383

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2443

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2503

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2563

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2623

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2624 GTGGAGGAAGATGGCTTCAAT 2644


RESULT 5
US-09-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-92

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512
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Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 6
US-09-984-827-93
; Sequence 93, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-93

  Query Match            99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity  99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 7
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-94

  Query Match            99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity  99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
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Db   2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 8
US-09-984-827-95
; Sequence 95, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-95

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 9
US-09-984-827-96
; Sequence 96, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-96

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773
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RESULT 10
US-09-984-827-97
; Sequence 97, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-97

Query Match 99.7%; Score 499.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 3.8e-154;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572
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Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773
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RESULT 11
US-09-984-827-98
; Sequence 98, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-98

Query Match 99.7%; Score 499.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 3.8e-154;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
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Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 12
US-09-984-827-99
; Sequence 99, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-99

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy    361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy    421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy    481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db   2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 13
US-09-984-827-100
; Sequence 100, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-100

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy     61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy    121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy    181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy    241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy    301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632
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Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 14
US-09-984-827-103
; Sequence 103, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-103

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
           |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773


RESULT 15
US-09-984-827-104
; Sequence 104, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-104

  Query Match             99.7%;  Score 499.4;  DB 9;  Length 9870;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-154;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 2332

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    2333 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 2392

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2452

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 2512

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
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Db    2633 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 2752

Qy     481 GTGGAGGAAGATGGCTTCAAT 501
          |||||||||||||||||||||
Db    2753 GTGGAGGAAGATGGCTTCAAT 2773
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Job time : 64.6923 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 566.323 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_2250_2750
Perfect score: 501
Sequence: 1 gtgatcatcaagggcatcgt.....tggaggaagatggcttcaat 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	490	97.8	809	13	BI754756	BI754756 603025477
	2	285.8	57.0	324	10	AW845151	AW845151 RC0-CT000
c	3	242	48.3	333	9	AI344681	AI344681 qp09h03.x
	4	228.8	45.7	491	12	BF879888	BF879888 RC2-ET018
	5	205.4	41.0	427	13	BM153383	BM153383 TCBAP2D11
c	6	196.6	39.2	351	12	BF928185	BF928185 CM4-NT021
	7	186	37.1	2640	11	U66691	U66691 Homo sapien
c	8	164.2	32.8	850	14	W29003	W29003 55g7 Human
	9	156.4	31.2	833	17	CNS032BC	AL224625 Tetraodon
c	10	142	28.3	1119	17	CNS03S5G	AL258109 Tetraodon
	11	120.4	24.0	670	17	AZ721290	AZ721290 RPCI-24-9
	12	101	20.2	375	12	BF928780	BF928780 IL5-NT022
c	13	96.4	19.2	969	17	CNS03ZVK	AL268121 Tetraodon
	14	93.6	18.7	732	12	BF608713	BF608713 MY1_00165
	15	91.8	18.3	408	9	AA772600	AA772600 ai30h01.s
	16	90.2	18.0	476	12	BF516223	BF516223 UI-H-BW1-
	17	89	17.8	475	14	BQ346986	BQ346986 QV4-NT024
	18	85.6	17.1	1009	17	CNS03EXW	AL240989 Tetraodon
	19	83	16.6	986	14	BQ921813	BQ921813 AGENCOURT
c	20	82	16.4	950	17	CNS04ZPQ	AL314567 Tetraodon
	21	79	15.8	672	17	BH260053	BH260053 CH230-90D
c	22	77.4	15.4	956	17	CNS03OKO	AL253473 Tetraodon
	23	76.8	15.3	564	17	FR0029378	AL025749 Fugu rubr
	24	75.2	15.0	379	9	AI050892	AI050892 ow31g08.s
c	25	74.6	14.9	191	13	BI039809	BI039809 IL3-NT028
c	26	72.6	14.5	210	17	CNS03ZVJ	AL268120 Tetraodon
	27	71.6	14.3	1032	13	BI659235	BI659235 603301621
	28	69.8	13.9	729	13	BI330649	BI330649 602981095
	29	65	13.0	404	12	BG152462	BG152462 naf55d08.
	30	63.8	12.7	317	12	BF922869	BF922869 QV4-NT024
c	31	63.8	12.7	831	17	AQ747504	AQ747504 HS_5536_A
c	32	63.6	12.7	999	17	CNS03IS9	AL245970 Tetraodon
c	33	62.2	12.4	825	17	CNS04KMC	AL295005 Tetraodon
c	34	61.4	12.3	913	17	CNS03NGC	AL252021 Tetraodon
c	35	61.4	12.3	925	17	CNS041M7	AL270376 Tetraodon
	36	58.6	11.7	1093	17	CNS02AFG	AL188485 Tetraodon
c	37	58.4	11.7	1107	14	BQ708777	BQ708777 AGENCOURT
c	38	57.4	11.5	589	17	FR0029372	AL025743 Fugu rubr
	39	56.2	11.2	878	17	CNS055PI	AL322335 Tetraodon
c	40	56.2	11.2	1003	17	CNS03SE9	AL258426 Tetraodon
c	41	56	11.2	1087	17	CNS0556V	AL321664 Tetraodon
	42	54.4	10.9	340	17	AZ305988	AZ305988 1M0006E21
c	43	52.6	10.5	487	17	AQ846043	AQ846043 LMAJFV1_1
	44	51.8	10.3	349	14	BQ344563	BQ344563 QV4-NT024
	45	51	10.2	571	12	BF189018	BF189018 234266 MA

ALIGNMENTS

RESULT 1
BI754756
LOCUS BI754756 809 bp mRNA linear EST 25-SEP-2001
DEFINITION 603025477F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195995 5', mRNA sequence.
ACCESSION BI754756
VERSION BI754756.1 GI:15746334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 809)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11490 row: i column: 20
High quality sequence stop: 768.
FEATURES Location/Qualifiers
source 1. .809

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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5195995"
                     /clone_lib="NIH_MGC_114"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is  destroyed
                     upon cloning).  Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      151 a    199 c    220 g    239 t
ORIGIN

  Query Match             97.8%;  Score 490;  DB 13;  Length 809;
  Best Local Similarity   99.8%;  Pred. No. 8.3e-123;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
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Db     133 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 192

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 252

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 312

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 372

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGGCATCATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGGCATCATC 432

Qy     301 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 492

Qy     361 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     493 ACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 552

Qy     421 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 480
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Db     553 TTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCT 612

Qy     481 GTGG-AGGAAGATGGCTTCAAT 501
           |||| ||||||||||||||||||
Db     613 GTGGAAGGAAGATGGCTTCAAT 634


RESULT 2
AW845151
LOCUS       AW845151                 324 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  RC0-CT0009-310599-024 CT0009 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW845151
VERSION     AW845151.1  GI:7940668
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC0-CT0009-310
            599-024&t3=1999-05-31&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 16
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0009"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       60 a     85 c     88 g     91 t
ORIGIN

  Query Match             57.0%;  Score 285.8;  DB 10;  Length 324;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-67;
  Matches  287;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 95

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
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Db      96 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 155

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 215

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 240
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Db     216 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGC 275

Qy     241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTG 289
          ||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     276 TTCCTGATTAGCACACTCTTCTCCAGAGCCCACCTGGCAGCAGCCTGTG 324


RESULT 3
AI344681/c
LOCUS       AI344681                 333 bp    mRNA    linear   EST 02-FEB-1999
DEFINITION  qp09h03.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917557 3'
            similar to SW:ABC1_MOUSE P41233 ATP-BINDING CASSETTE TRANSPORTER 1.
            ;, mRNA sequence.
ACCESSION   AI344681
VERSION     AI344681.1  GI:4081887
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 333)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 432   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .333
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1917557"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       94 a     84 c     89 g     66 t
ORIGIN

  Query Match             48.3%;  Score 242;  DB 9;  Length 333;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-55;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    137 TGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGT 196
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Db    333 TGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGT 274

Qy    197 TTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACAC 256
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Db    273 TTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACAC 214

Qy    257 TCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACC 316
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Db    213 TCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACC 154

Qy    317 TGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCG 376
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Db    153 TGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCG 94

Qy    377 CT 378
          ||
Db     93 CT 92


RESULT 4
BF879888
LOCUS       BF879888                491 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  RC2-ET0188-281100-013-g12 ET0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF879888
VERSION     BF879888.1  GI:12270092
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2&t2=RC2-ET0188-
            281100-013-g12&t3=2000-11-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 489.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="ET0188"
                     /dev_stage="Adult"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      119 a    114 c    122 g    136 t
ORIGIN

  Query Match             45.7%;  Score 228.8;  DB 12;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-51;
  Matches  230;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    270 CAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCT 329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 CAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCT 72

Qy    330 GTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTC 132

Qy    390 TCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 449
          ||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Db    133 TCCTGTGGCTTTGGGGTTGGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGG 192

Qy    450 AGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 501
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Db    193 AGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 244


RESULT 5
BM153383
LOCUS       BM153383                427 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  TCBAP2D11628 Pediatric pre-B cell acute lymphoblastic leukemia
            Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1162, mRNA
            sequence.
ACCESSION   BM153383
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VERSION     BM153383.1  GI:17178477
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
            Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
  TITLE     Pediatric Leukemia cDNA Sequencing Project (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Judith F. Margolin
            Texas Children's Cancer Center and Human Genome Sequencing Center
            at Baylor College of Medicine
            1102 Bates, MC3-3320 Houston, TX 77030, USA
            Tel: 832-824-4536
            Fax: 832-825-4038
            Email: clones@txccc.org
            Seq primer: M13 primer.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="TCBAP1162"
                     /clone_lib="Pediatric pre-B cell acute lymphoblastic
                     leukemia Baylor-HGSC project=TCBA"
                     /sex="male"
                     /tissue_type="leukopheresis"
                     /cell_type="pre-B cell"
                     /dev_stage="pediatric 2 years"
                     /lab_host="DH10B"
                     /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
                     First strand cDNA was primed with an anchored
                     XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN
                     3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
                     was primed with a BamHI-dC primer
                     [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
                     Double-stranded cDNA was then digested with BamHI and XhoI
                     and directionally cloned into the BamHI and SalI sites of
                     lambda pSB vector. Library went through one round of
                     normalization. Library was constructed by Wei Yu at RIKEN
                     of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
                     Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
                     Schneider C, Hayashizaki Y, High efficiency selection of
                     full-length cDNA by improved biotinylated cap trapper.,
                     DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT       85 a    104 c    126 g    112 t
ORIGIN

  Query Match           41.0%;  Score 205.4;  DB 13;  Length 427;
  Best Local Similarity  99.5%;  Pred. No. 2.4e-45;
  Matches  206;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 280

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     281 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 340

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 400

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTG 207
          |||||||||||||||||||||||||||
Db     401 GATCCCAGCGTGGTGTTTGTCTTCCTG 427


RESULT 6
BF928185/c
LOCUS       BF928185                351 bp    mRNA    linear   EST 19-JAN-2001
DEFINITION  CM4-NT0213-061200-488-e08 NT0213 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF928185
VERSION     BF928185.1  GI:12326313
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM4&t2=CM4-NT0213-
            061200-488-e08&t3=2000-12-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 3
            High quality sequence stop: 351.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NT0213"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       95 a     97 c     87 g     72 t
ORIGIN

  Query Match           39.2%;  Score 196.6;  DB 12;  Length 351;
  Best Local Similarity  97.7%;  Pred. No. 5.5e-43;
  Matches  210;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATC 161

Qy      61 ATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     160 ATGGGCCTGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTT 101

Qy     121 CTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     100 CTTGTGAGCGCT-GCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 42

Qy     181 GATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTT 215
          |||||||||||||||  ||||||| |||||||||
Db      41 GATCCCAGCGTGGTGTAAGTCTTCCGGTCCGTGTT 7


RESULT 7
U66691
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LOCUS       U66691                  2640 bp    mRNA    linear   HTC 23-JUL-2001
DEFINITION  Homo sapiens clone EST394388 mRNA sequence.
ACCESSION   U66691
VERSION     U66691.1  GI:1906576
KEYWORDS    HTC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2640)
  AUTHORS   Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
  TITLE     Characterization of the human ABC superfamily: isolation and
            mapping of 21 new genes using the expressed sequence tags database
  JOURNAL   Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
  MEDLINE   97049974
   PUBMED   8894702
REFERENCE   2  (bases 1 to 2640)
  AUTHORS   Allikmets,R., Gerrard,B. and Dean,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Human Genetics Section, National Cancer
            Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
     source          1. .2640
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="EST394388"
                     /note="similar to ATP-binding cassette transporter"
BASE COUNT      607 a    672 c    667 g    647 t     47 others
ORIGIN

  Query Match           37.1%;  Score 186;  DB 11;  Length 2640;
  Best Local Similarity  59.6%;  Pred. No. 1.4e-39;
  Matches  297;  Conservative    0;  Mismatches  201;  Indels    0;  Gaps    0;

Qy       2 TGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCA 61
Db      41 TGNCTGTGAAGAGCATCGACTATGAGAAGGAGTTGCGACTGAAGGAGACCTTGAAAAATC 100

Qy      62 TGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTC 121
Db     101 AGGGTGTCTCCAATCCAGTGANTTGTTGTACCTGGTTCCTGGACANCTTCTCCATCATGT 160

Qy     122 TTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTG 181
Db     161 CGATGANCATCTTCCTCCTGCCGATATTCATCATACATGGNAGAATCCNACATTACANCG 220

Qy     182 ATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCT 241
Db     221 ACCCANTCATCCTCTTCCTGTTCTTGTTGGCTTTCTCCACTGCCACCATCATGCTGTGCT 280

Qy     242 TCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCT 301
Db     281 TTCTGCTCAGCACCTTCTTCTCCAAGNCCAGTCTGGCANCAGCCTGTAGTGGTGTCATCT 340

Qy     302 ACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCA 361
Db     341 ATTTCACCCTCTACCTCCCACACATCCTGTGCNTCGCCTGGCAGGACCGCATGACCCCTG 400

Qy     362 CACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACT 421
Db     401 AGCTGNAGNAGGCTGTGAGCTTNCTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTGCC 460

Qy     422 TTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTG 481
Db     461 TGGTTCGCNTTGAAGAGCAAGGCCTGGGGCTGCAGTGGANCAACATCGGGAACAGTCCCA 520

Qy     482 TGGAGGAAGATGGCTTCA 499
Db     521 CGGAAGGGGACGAATTCA 538


RESULT 8
W29003/c
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LOCUS       W29003                  850 bp    mRNA    linear   EST 08-MAY-1996
DEFINITION  55g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
            , mRNA sequence.
ACCESSION   W29003
VERSION     W29003.1  GI:1309023
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 850)
  AUTHORS   Macke, J., Smallwood, P. and Nathans, J.
  TITLE     Adult Human Retina cDNA
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Dr. Jeremy Nathans
            Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
            Johns Hopkins School of Medicine
            725 North Wolfe Street, Baltimore, MD 21205
            Tel: 410 955 4678
            Fax: 410 614 0827
            Email: jeremy_nathans@qmail.bs.jhu.edu
            Clones from this library are NOT available.
            PCR PRimers
            FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
            BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
            Seq primer: GGGTAAAAAGCAAAAGAATT.
FEATURES             Location/Qualifiers
     source          1. .850
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human retina cDNA randomly primed sublibrary"
                     /sex="mixed (males and females)"
                     /tissue_type="retina"
                     /dev_stage="adult"
                     /lab_host="E. coli strain K802"
                     /note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI;
                     Site_2: EcoRI; The library used for sequencing was a
                     sublibrary derived from a human retina cDNA library.
                     Inserts from retina cDNA library DNA were isolated,
                     randomly primed, PCR amplified, size-selected, and cloned
                     into lambda gt10.  Individual plaques were arrayed and
                     used as templates for PCR amplification, and these PCR
                     products were used for sequencing."
BASE COUNT      205 a    199 c    224 g    174 t     48 others
ORIGIN

  Query Match           32.8%;  Score 164.2;  DB 14;  Length 850;
  Best Local Similarity  59.2%;  Pred. No. 6.3e-34;
  Matches  282;  Conservative    0;  Mismatches  193;  Indels    1;  Gaps    1;

Qy      24 TGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATACT 83
Db     578 TGAGAAGGAGTTGCGACTG-AGGAGACCTTGAAAAATCAGGGTGTCTCCAATCCAGTGAN 520

Qy      84 CTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTGCTAGT 143
Db     519 TTGTTGTACCTGGTTCCTGGACANCTTCTCCATCATGTCGATGANCATCTTCCTCCTGCC 460

Qy     144 GGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTT 203
Db     459 GATATTCATCATACATGGNAGAATCCNACATTACANCGACCCANTCATCCTCTTCCTGTT 400

Qy     204 CCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTC 263
Db     399 CTTGTTGGCTTTCTCCACTGCCACCATCATGCTGTGCTTTCTGCTCAGCACCTTCTTCTC 340

Qy     264 CAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTA 323
Db     339 CAAGNCCAGTCTGGCANCAGCCTGTAGTGGTGTCATCTATTTCACCCTCTACCTCCCACA 280

Qy     324 CGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGCCT 383
Db     279 CATCCTGTGCNTCGCCTGGCAGGACCGCATGACCCCTGAGCTGNAGNAGGCTGTGAGCTT 220
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Qy    384 GCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGG 443
          |||||||| ||||| ||||| ||||||  ||||| | | |  |   |||| ||||| ||
Db    219 NCTGTCTCCGGTGGCATTTGGATTTGGCACTGAGTGCCTGGTTCGCNTTGAAGAGCAAGG 160

Qy    444 CATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCA 499
          | | ||  |||||||  |||| |    | |||||   ||| |  || |  ||||
Db    159 CCTGGGGCTGCAGTGGANCAACATCGGGAACAGTCCCACGGAAGGGGACGAATTCA 104
```

RESULT 9
CNS032BC
LOCUS CNS032BC 833 bp DNA linear GSS 15-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 206J21 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL224625
VERSION AL224625.1 GI:7883494
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 833)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 833)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 833)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .833
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="206J21"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG206CE11SP1~end : PUC-Ori"
BASE COUNT 134 a 252 c 258 g 187 t 2 others
ORIGIN

Query Match 31.2%; Score 156.4; DB 17; Length 833;
Best Local Similarity 64.5%; Pred. No. 8.3e-32;
Matches 294; Conservative 1; Mismatches 82; Indels 79; Gaps 1;

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Qy     13 GGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGAC 72
          || |  || |||||||||||||  |||||| |||||||| |||||||||| ||| ||
Db      1 GGAAAGGTCTATGAGAAGGAGGCCAGGCTGAAGGAGACCATGAGGATCATGGGACTGAAC 60

Qy     73 AACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCT 132
          ||| |||| || ||||  |||||||||| || |||||  |||||| ||  | ||||||
Db     61 AACGGCATCCTGTGGTGCAGCTGGTTCATCAGCAGCCTGGTTCCTCTCCTGTTCAGCGCT 120

Qy    133 GGCCTGCTAGTGGTCATCCTGAAGTT---------------------------------- 158
          || ||||| ||| |  | || :|| |
Db    121 GGACTGCTGGTGCTGCTGCTYWAGGTGAGAAGGTCTTTTCTCGGGAGGTTCTTGGGAACC 180
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```
Qy    159 ----------------------------------------------AGGAAACCTGCTGCC 173
                                                         ||| ||||||||||
Db    181 GGGTCCAGAACCAGACTCCACCAGGCTCTTCTGTGTCCGTCAGAAAGGGAACCTGCTGCC 240

Qy    174 CTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCT 233
          |||||| || ||  | ||||| ||  |||||||| ||    |  |||||||||| ||| |
Db    241 CTACAGCGACCCAGGGGTGGTCTTCCTCTTCCTGGCCTCCTACGCTGTGGTGACCATCAT 300

Qy    234 GCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGG 293
          |||||||||||||| | |||||   ||||||| | |||||||||| || |||||||| ||
Db    301 GCAGTGCTTCCTGCTCAGCACGGCCTTCTCCCGGGCCAACCTGGCGGCGGCCTGTGGCGG 360

Qy    294 CATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGT 353
          |||||||||||||| || |||||||||||||| || || ||||| ||| |||||||| |
Db    361 GATCATCTACTTCACCCTCTACCTGCCCTACGTGCTCTGCGTGGCCTGGGAGGACTACAT 420

Qy    354 GGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTC 389
          |||||| ||  |||  |  | |||     | ||||
Db    421 CGGCTTCTCAGCCAAAGTTGTTGCTGTAAGGGTGTC 456
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RESULT 10
CNS03S5G/c
LOCUS CNS03S5G 1119 bp DNA linear GSS 17-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 051A03 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL258109
VERSION AL258109.1 GI:7979121
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1119)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1119)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1119)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .1119
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="051A03"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG051AA02SP1~end : PUC-Ori"
BASE COUNT 239 a 351 c 341 g 185 t 3 others
ORIGIN

Query Match 28.3%; Score 142; DB 17; Length 1119;
Best Local Similarity 64.2%; Pred. No. 8.4e-28;
Matches 290; Conservative 1; Mismatches 81; Indels 80; Gaps 2;

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Qy       2 TGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCA 61
Db    1095 TCATCCTGAAGAGCGTGGTCTATGAGAAGGAGGC-CAGCTGAAGGAGACCATGAGGATCA 1037

Qy      62 TGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTC 121
Db    1036 TGGGACTGAACAACGGCATCCTGTGGTGCAGCTGGTTCATCAGCAGCCTGGTYCCTCTCC 977

Qy     122 TTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTT---------------------- 158
Db     976 TGATCAGCGCTGGACTGCTGGTGCTGCTGCTCAAGGTGAGAAGGTCTTTTCTCGGGAGGT 917

Qy     159 ------------------------------------------------------AGGA 162
Db     916 TCTTGGGAACCGGGTCCAGAACCGGGCTCCACCAGGCTCTTCTGTGTCCGTCAGAAAGGG 857

Qy     163 AACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTG 222
Db     856 AACCTGCTGCCCTACAGCGACCCAGGGGTGGTCTTCCTCTTCCTGGCCTCCTACGCTGTG 797

Qy     223 GTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCA 282
Db     796 GTGACCATCATGCAGTGCTTCCTGCTCAGCACGGCCTTCTCCCGGGCCAACCTGGCGGCG 737

Qy     283 GCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGG 342
Db     736 GCCTGTGGCGGGATCATCTACTTCACCCTCTACCTGCCCTACGTGCTCTGCGTGGCCTGG 677

Qy     343 CAGGACTACGTGGGCTTCACACTCAAGATCTT 374
Db     676 GAGGACTACATCGCTTCTCAGCCAAAGTTGTT 645
```

RESULT 11
AZ721290
LOCUS AZ721290 670 bp DNA linear GSS 24-JAN-2001
DEFINITION RPCI-24-93E12.TV RPCI-24 Mus musculus genomic clone RPCI-24-93E12, DNA sequence.
ACCESSION AZ721290
VERSION AZ721290.1 GI:12463834
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 670)
AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-24-93E12.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 93 row: E column: 12
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .670
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-93E12"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT 160 a 163 c 158 g 189 t
ORIGIN

Query Match 24.0%; Score 120.4; DB 17; Length 670;
Best Local Similarity 89.2%; Pred. No. 4.9e-22;
Matches 141; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Qy     151 CTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCC 210
Db     513 CTCCAGTTAGGAAACCTGCTGCCCTATAGTGACCCCAGCGTGGTGTTCGTCTTCCTGTCT 572

Qy     211 GTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCC 270
Db     573 GTGTTTGCCATGGTGACCATCCTACAGTGCTTTCTCATTAGCACGCTCTTCTTCCGTGCC 632

Qy     271 AACCTGGCAGCAG-CCTGTGGGGGGCATCATCTACTTCA 307
Db     633 AACCTGGCAGCAGCCCTGTGGGGGCATCATCTACTTCA 670
```

RESULT 12
BF928780
LOCUS BF928780 375 bp mRNA linear EST 19-JAN-2001
DEFINITION IL5-NT0228-061200-308-g05 NT0228 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF928780
VERSION BF928780.1 GI:12326908
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-NT0228-061200-308-g05&t3=2000-12-06&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 331.
FEATURES Location/Qualifiers
source 1. .375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0228"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 64 a 113 c 106 g 92 t
ORIGIN

Query Match 20.2%; Score 101; DB 12; Length 375;
Best Local Similarity 56.9%; Pred. No. 6.8e-17;
Matches 185; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy      52 ATGCGGATCATGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTC 111
           ||| || |||||||||| |||||    | | |||| |   ||||||||| |   || |
Db       3 ATGAAGACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTT 62

Qy     112 ATTCCTCTTCTTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTG 171
           | |  ||      |   ||         ||    | ||||||||||  ||  |  ||||
Db      63 GTGCAGCTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTT 122

Qy     172 CCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATC 231
           ||||  |       | |  | |  |||||||| | || |  || ||||  || |||
Db     123 ATGCACAGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATC 182

Qy     232 CTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGG 291
           ||   ||||||||| |       || | |||||  ||||| |||||  | ||||| ||
Db     183 ATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGT 242

Qy     292 GGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTAC 351
           ||||||||||||||||  |  ||| |||||||| |       | |    |  ||||
Db     243 GGCATCATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTG 302

Qy     352 GTGGGCTTCACACTCAAGATCTTCG 376
           | |      |   ||| |  |||||
Db     303 GCGCATGATAAGATCACGGCCTTCG 327
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RESULT 13
CNS03ZVK/c
LOCUS CNS03ZVK 969 bp DNA linear GSS 18-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 071A24 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL268121
VERSION AL268121.1 GI:7989956
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 969)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 969)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 969)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .969
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="071A24"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG071BA12LP2-end : T7"
BASE COUNT 260 a 231 c 264 g 209 t 5 others
ORIGIN

Query Match 19.2%; Score 96.4; DB 17; Length 969;
Best Local Similarity 67.6%; Pred. No. 2.1e-15;
Matches 150; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

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Qy     155 AGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGT 214
           |||  ||   | | || |  ||||| || |||    |  | ||  ||||||||   || |
Db     352 AGTACGGCGGCGTCCTCCAGTACAGCGACCCCTCGCTCATCTTCCTCTTCCTGCTGGTCT 293

Qy     215 TTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACC 274
           |     |||  || |||   |||||||||||| ||||||    |||||||| ||||||||
Db     292 TCTGCCTGGCCACCATCACTCAGTGCTTCCTCATTAGCGTCTTCTTCTCCAAAGCCAACT 233

Qy     275 TGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTG 334
           ||||||| || || || ||| ||||||||||   || |||||||| |||||||| |||
Db     232 TGGCAGCGGCGTGCGGCGGCCTCATCTACTTCGTCCTCTACCTGCCGTACGTCCTTTGT- 174

Qy     335 TGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCG 376
           || |||   |||  | ||||||||  |   ||||  |   ||
Db     173 ACGCCTGGAGCGACGTCATGGGCTTCCCCGCCAAGGTTGCCG 132
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RESULT 14
BF608713
LOCUS BF608713 732 bp mRNA linear EST 01-APR-2001
DEFINITION MY1_001655 Mouse 9-day fetus cDNA library ICRFp522 Mus musculus cDNA clone ICRFp5220032 5', mRNA sequence.
ACCESSION BF608713
VERSION BF608713.1 GI:13505205
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 732)
AUTHORS Yahyawi,M., Hennig,S., Neidhardt,L., Radelof,U., Hermann,B.G., Lehrach,H. and O'Brien,J.
TITLE Detection of a high number of novel genes in a 9-day mouse embryo cDNA library normalised by oligonucleotide fingerprinting
JOURNAL Unpublished (2001)
COMMENT Contact: Hennig S
laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
EST's are made from clones being representatives of clone clusters. Clone clusters were calculated from oligonucleotide fingerprints.
PCR PRimers
FORWARD: 5'-GAGCTATTCCAGAAGTAGTGA-3'
BACKWARD: 5'-TAATACGACTCACTATAGGG-3'
Seq primer: 5'-ATTTAGGTGACACTATAG-3'
High quality sequence stop: 732.
FEATURES Location/Qualifiers
source 1. .732
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="ICRFp5220032"
/clone_lib="Mouse 9-day fetus cDNA library ICRFp522"
/tissue_type="whole embryo"
/dev_stage="embryonic 9-day"
/lab_host="E.coli, XL1 blue"

/note="Vector: PSVSport1; Site_1: NotI; Site_2: SalI; Library preparation by oligo_dT priming of RNA. Clones can be ordered from the Resource Center in Berlin, http://www.rzpd.de."

BASE COUNT 159 a 221 c 157 g 192 t 3 others
ORIGIN

Query Match 18.7%; Score 93.6; DB 12; Length 732;
Best Local Similarity 51.6%; Pred. No. 1e-14;
Matches 247; Conservative 0; Mismatches 217; Indels 15; Gaps 1;

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Qy       4 ATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATG 63
Db     249 ATCATCCGGGCTGTGGTGCAGGAGAAGGAGAAAAAACTAAAGGAGTACATGCGCATGATG 308

Qy      64 GGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTT 123
Db     309 GGGCTTAACAGCTGGCTACACTGGAGCGCTTGGTTCCTCATGTTCTTCCTATTCTTCCTC 368

Qy     124 GTGAGCGCTGGCCTGCTAGTGGTCATCCT--------------GAAGTTAGGAAACCTG 168
Db     369 ATCGTGGTCTCCTTCATGACGCTNCTGTTCTGTGTCAAAGTGAAGAAGGACATAGCAGTC 428

Qy     169 CTGCCCTACAGTGATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACA 228
Db     429 CTTTCCAACAGCGACCCCTCCCTGGTCCTGGCGTTCCTGCTGTGTTTTGCAATCTCCTCC 488

Qy     229 ATCCTGCAGTGCTTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGT 288
Db     489 ATTTCCTTCAGCTTCATGGTCAGCACCTTCTTCAGTAAAGCCAACATAGCAACAGCCGTG 548

Qy     289 GGGGGCATCATCTACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGAC 348
Db     549 GGTGGCTTCCTGTACTTCTTCACCTATACCCCCTACTTTTTCGTGGCTCCTCGGTACAAC 608

Qy     349 TACGTGGGCTTCACACTCAAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTT 408
Db     609 TGGATGACACTGAGTCAAAAGCTCTTGTCCTGTCTCCTATNCTATGTTGCCATGGCAATG 668

Qy     409 GGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCT 467
Db     669 GGAGCCCAGCTCATAGGANAATTCGAAGCCAAAGGCACTGGCATCCAGTGGCGGGACCT 727
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RESULT 15
AA772600
LOCUS AA772600 408 bp mRNA linear EST 31-DEC-1998
DEFINITION ai30h01.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1358545 3' similar to SW:ABC1_MOUSE P41233 ATP-BINDING CASSETTE TRANSPORTER 1. ;, mRNA sequence.
ACCESSION AA772600
VERSION AA772600.1 GI:2824383
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 408)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand

Insert Length: 762 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 388.

FEATURES Location/Qualifiers
source 1. .408
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1358545"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

BASE COUNT 75 a 122 c 117 g 93 t 1 others
ORIGIN

Query Match 18.3%; Score 91.8; DB 9; Length 408;
Best Local Similarity 58.5%; Pred. No. 2.3e-14;
Matches 159; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

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Qy       2 TGATCATCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCA 61
Db     137 TGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCA 196

Qy      62 TGGGCCTGGACAACAGCATACTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTC 121
Db     197 TGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGT 256

Qy     122 TTGTGAGCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTG 181
Db     257 CCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCC 316

Qy     182 ATCCCAGCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCT 241
Db     317 ACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCT 376

Qy     242 TCCTGATTAGCACACTCTTCTCCAGAGCCAAC 273
Db     377 TCCTGGTGTCTGTGCTGTACTCAAGNGCAAGC 408
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Search completed: April 3, 2003, 16:36:47
Job time : 577.323 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 992.885 Seconds
(without alignments)
14684.987 Million cell updates/sec

Title: US-09-595-526C-1_COPY_4750_5250
Perfect score: 501
Sequence: 1 cacaaagaaaacaaaacact.....tctgatgaccacatcagtgg 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	501	100.0	7860	6	AX092594	AX092594 Sequence
2	501	100.0	7862	6	AX135712	AX135712 Sequence
3	501	100.0	10442	6	AX060713	AX060713 Sequence
4	501	100.0	10442	6	AX060892	AX060892 Sequence
5	501	100.0	10442	9	AF285167	AF285167 Homo sapi
6	501	100.0	10474	6	AX060719	AX060719 Sequence
7	501	100.0	10474	6	AX060721	AX060721 Sequence
8	501	100.0	10474	6	AX060898	AX060898 Sequence
9	501	100.0	10474	6	AX060900	AX060900 Sequence
10	499.4	99.7	6786	9	AB055982	AB055982 Homo sapi
11	497.8	99.4	6880	6	AX253450	AX253450 Sequence
12	497.8	99.4	6880	9	HSA012376	AJ012376 Homo sapi
13	497.8	99.4	7260	6	AX253452	AX253452 Sequence
14	497.8	99.4	9495	6	AX059978	AX059978 Sequence
15	497.8	99.4	9497	6	AX059973	AX059973 Sequence
16	497.8	99.4	9497	9	AF165281	AF165281 Homo sapi
17	497.8	99.4	9593	6	AX059976	AX059976 Sequence
18	497.8	99.4	9741	6	AX127830	AX127830 Sequence
19	497.8	99.4	9741	6	AX139817	AX139817 Sequence
20	497.8	99.4	9741	6	AX351038	AX351038 Sequence
21	497.8	99.4	9854	6	AX127831	AX127831 Sequence
22	497.8	99.4	9854	6	AX139818	AX139818 Sequence
23	409.8	81.8	7878	10	MMABC1	X75926 Mus musculu
24	336.2	67.1	7074	5	AF362377	AF362377 Gallus ga
25	173	34.5	190	9	HSATPCB22	AF165303 Homo sapi
26	173	34.5	645	6	AX059890	AX059890 Sequence
c 27	173	34.5	129608	9	AL353685	AL353685 Human DNA
28	173	34.5	183999	6	AX092589	AX092589 Sequence
29	173	34.5	201144	9	AF287262	AF287262 Homo sapi
30	172.6	34.5	149034	9	AF275948	AF275948 Homo sapi
31	170	33.9	170	6	AX059921	AX059921 Sequence
32	165	32.9	7298	9	AF001945	AF001945 Homo sapi
33	163.4	32.6	7276	9	HSU88667	U88667 Human ATP b
34	163.4	32.6	7323	9	HSAF000148	AF000148 Homo sapi
35	155.4	31.0	7268	10	MMAF000149	AF000149 Mus muscu
36	153.8	30.7	7709	4	BTU90126	U90126 Bos taurus
37	152.2	30.4	186889	2	AL807243	AL807243 Mus muscu
38	152.2	30.4	206695	2	AC091466	AC091466 Mus muscu
39	152.2	30.4	230272	2	AL772397	AL772397 Mus muscu
40	150.6	30.1	278572	10	AF287263	AF287263 Mus muscu
41	139.4	27.8	5669	6	AX202220	AX202220 Sequence
42	139.4	27.8	6522	6	AX202218	AX202218 Sequence
43	137.8	27.5	6027	9	AB055390	AB055390 Homo sapi
44	137.8	27.5	6432	6	AX320364	AX320364 Sequence
45	137.8	27.5	6588	9	AF250238	AF250238 Homo sapi

ALIGNMENTS

RESULT 1
AX092594
LOCUS AX092594 7860 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 6 from Patent WO0115676.
ACCESSION AX092594
VERSION AX092594.1 GI:13444651
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7860)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels

```
  JOURNAL   Patent: WO 0115676-A 6 08-MAR-2001;
            University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .7860
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2014 a   1860 c   2008 g   1978 t
ORIGIN
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Query Match 100.0%; Score 501; DB 6; Length 7860;
Best Local Similarity 100.0%; Pred. No. 9.7e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db    4534 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4593

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4594 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4653

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4654 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4713

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4714 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4773

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4774 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4833

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4834 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4893

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4894 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4953

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4954 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5013

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5014 CTCTGATGACCACATCAGTGG 5034
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RESULT 2
AX135712
LOCUS       AX135712               7862 bp    DNA     linear   PAT 29-MAY-2001
DEFINITION  Sequence 1 from Patent WO0132184.
ACCESSION   AX135712
VERSION     AX135712.1  GI:14271961
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7862)
  AUTHORS   Attie,A.D., Cook,M., Gray-Keller,M.P., Hayden,M.R., Pimstone,S. and
            Brooks-Wilson,A.
  TITLE     Abc1 modulation for the modulation of cholesterol transport
  JOURNAL   Patent: WO 0132184-A 1 10-MAY-2001;
            WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .7862
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                     /db_xref="taxon:9606"
BASE COUNT     2013 a   1861 c   2010 g   1978 t
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Query Match 100.0%; Score 501; DB 6; Length 7862;
Best Local Similarity 100.0%; Pred. No. 9.7e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db    4596 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4655

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Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    4836 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4895

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5016 CTCTGATGACCACATCAGTGG 5036
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RESULT 3
AX060713
LOCUS       AX060713               10442 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078972.
ACCESSION   AX060713
VERSION     AX060713.1  GI:12406103
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 1 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2898 a   2297 c   2408 g   2835 t      4 others
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Query Match 100.0%; Score 501; DB 6; Length 10442;
Best Local Similarity 100.0%; Pred. No. 9.8e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db    4990 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5049

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    5050 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5109

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Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db    5170 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5229

Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5230 CTCTGATGACCACATCAGTGG 5250
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RESULT 4
AX060892
LOCUS       AX060892               10442 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078971.
ACCESSION   AX060892
VERSION     AX060892.1  GI:12406270
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 1 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10442
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2898 a    2297 c    2408 g    2835 t      4 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 10442;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-138;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Db    4870 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4929

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db    4930 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4989

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Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    5050 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5109

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Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db    5170 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5229

Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5230 CTCTGATGACCACATCAGTGG 5250
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RESULT 5
AF285167
LOCUS       AF285167               10442 bp    mRNA    linear   PRI 09-AUG-2000
DEFINITION  Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
            complete cds.
ACCESSION   AF285167
VERSION     AF285167.1  GI:9755158
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10442)
  AUTHORS   Schwartz,K., Lawn,R.M. and Wade,D.P.
  TITLE     ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
            regulated by LXR
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 10442)
  AUTHORS   Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
            Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
            3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES             Location/Qualifiers
     source          1. .10442
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                     /chromosome="9"
                     /map="9q31"
                     /cell_type="fibroblast"
                     /tissue_type="skin"
     gene            1. .10442
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     CDS             291. .7076
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BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 100.0%; Score 501; DB 9; Length 10442;
Best Local Similarity 100.0%; Pred. No. 9.8e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5230 CTCTGATGACCACATCAGTGG 5250
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RESULT 6
AX060719
LOCUS AX060719 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078972.
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES Location/Qualifiers
source 1. .10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 100.0%; Score 501; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 9.8e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db    4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5262 CTCTGATGACCACATCAGTGG 5282
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RESULT 7
AX060721
LOCUS AX060721 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS .
SOURCE human.

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2907 a   2304 c   2415 g   2844 t      4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-138;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db   4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db   5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Db   5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy    481 CTCTGATGACCACATCAGTGG 501
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Db   5262 CTCTGATGACCACATCAGTGG 5282


RESULT 8
AX060898
LOCUS       AX060898               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078971.
ACCESSION   AX060898
VERSION     AX060898.1  GI:12406275
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 7 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2906 a   2305 c   2416 g   2843 t      4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-138;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db   4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db   4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db   4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db   5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db   5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Db   5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db   5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   5262 CTCTGATGACCACATCAGTGG 5282


RESULT 9
AX060900
LOCUS       AX060900               10474 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 9 from Patent WO0078971.
ACCESSION   AX060900
VERSION     AX060900.1  GI:12406276
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10474)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 9 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2907 a   2304 c   2415 g   2844 t      4 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-138;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db   4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db   4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db   4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db   5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Db   5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy    481 CTCTGATGACCACATCAGTGG 501
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Db   5262 CTCTGATGACCACATCAGTGG 5282
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RESULT 10
AB055982
LOCUS       AB055982               6786 bp    mRNA    linear   PRI 18-AUG-2001
DEFINITION  Homo sapiens mRNA for ABCA1, complete cds.
ACCESSION   AB055982
VERSION     AB055982.1  GI:15212106
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tanaka,A.R., Abe-Dohmae,S., Arakawa,R., Sadanami,K., Kidera,A.,
            Kioka,N., Amachi,T., Yokoyama,S. and Ueda,K.
  TITLE     A new topological model of functional human ABCA1-Signal peptide
            cleavage and glycosylation of a large extracellular domain
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6786)
  AUTHORS   Ueda,K., Kioka,N. and Tanaka,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate
            School, Applied Life Sciences; Kitashirakawa, Kyoto Sakyo-ku, Kyoto
            606-8502, Japan (E-mail:uedak@kais.kyoto-u.ac.jp,
            Tel:81-75-753-6105, Fax:81-75-753-6104)
FEATURES             Location/Qualifiers
     source          1. .6786
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .6786
                     /gene="ABCA1"
     CDS             1. .6786
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                     /protein_id="BAB63210.1"
                     /db_xref="GI:15212107"
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                     NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
                     REKLAAAERVLRSNMDILKPILRTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMR
                     SWSDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
                     GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
                     RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
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                     KLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
                     NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQQMPY
                     PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
                     FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
                     SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCEYFALFE
                     EQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYIEAVFPGQYGIPRPW
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                     LQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
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                     TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVS
                     PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ
                     RILDGGGQNDILEIKELTKIYRRRKRPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM
                     LTGDTTVTRGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGV
                     PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
                     MDPKARRFLWNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLK
                     NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI
                     FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
                     SFLQDEKVKESYV"
BASE COUNT     1724 a   1643 c   1759 g   1660 t
ORIGIN

  Query Match           99.7%;  Score 499.4;  DB 9;  Length 6786;
  Best Local Similarity   99.8%;  Pred. No. 2.9e-137;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Db   4580 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4639

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db   4640 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4699

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db   4880 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 4939

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   4940 CTCTGATGACCACATCAGTGG 4960


RESULT 11
AX253450
LOCUS       AX253450               6880 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 1 from Patent WO0170810.
ACCESSION   AX253450
VERSION     AX253450.1  GI:16073978
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6880)
  AUTHORS   Schmitz,G. and Bodzioch,M.
  TITLE     Atp binding cassette transporter 1 (abc1) gene polymorphisms and
            uses thereof for the diagnosis and treatment of lipid,
            cardiovascular or inflammatory disorders
  JOURNAL   Patent: WO 0170810-A 1 27-SEP-2001;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .6880
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1760 a   1656 c   1783 g   1681 t
ORIGIN

  Query Match             99.4%;  Score 497.8;  DB 6;  Length 6880;
  Best Local Similarity   99.6%;  Pred. No. 8.6e-137;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db   4400 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4459

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db   4460 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4519

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Db   4520 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4579

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db   4640 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4699

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db   4760 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4819

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db   4820 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 4879

Qy     481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   4880 CTCCGATGACCACATCAGTGG 4900


RESULT 12
HSA012376
LOCUS       HSA012376              6880 bp    mRNA    linear   PRI 13-NOV-2001
DEFINITION  Homo sapiens mRNA for ATP-binding cassette transporter-1 (ABC-1).
ACCESSION   AJ012376
VERSION     AJ012376.1  GI:4128032
KEYWORDS    ABC-1 gene; ATP-binding cassette transporter-1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F.,
            Chimini,G., Kaminski,W.E. and Schmitz,G.
  TITLE     Molecular cloning of the human ATP-binding cassette transporter 1
            (hABC1): evidence for sterol-dependent regulation in macrophages
  JOURNAL   Biochem. Biophys. Res. Commun. 257 (1), 29-33 (1999)
  MEDLINE   99194549
   PUBMED   10092505
REFERENCE   2
  AUTHORS   Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F.,
            Chimini,G., Kaminski,W. and Schmitz,G.
  TITLE     Molecular Cloning of the Human ATP-Binding Cassette Transporter 1
            (hABC1): Evidence for Dterol-Dependent Regulation in Macrophages
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97, 7987-7992 (2000)
REFERENCE   3  (bases 1 to 6880)
  AUTHORS   Langmann,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Langmann T., Institute for Clinical
            Chemistry and Laboratory Medicine, University of Regensburg,
            Franz-Josef-Strauss-Allee 11, 93053, GERMANY
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Qy     481 CTCTGATGACCACATCAGTGG 501
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RESULT 13
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LOCUS       AX253452               7260 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 3 from Patent WO0170810.
ACCESSION   AX253452
VERSION     AX253452.1  GI:16073979
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7260)
  AUTHORS   Schmitz,G. and Bodzioch,M.
  TITLE     Atp binding cassette transporter 1 (abc1) gene polymorphisms and
            uses thereof for the diagnosis and treatment of lipid,
            cardiovascular or inflammatory disorders
  JOURNAL   Patent: WO 0170810-A 3 27-SEP-2001;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5260 CTCCGATGACCACATCAGTGG 5280


RESULT 14
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LOCUS       AX059978               9495 bp    DNA     linear   PAT 22-JAN-2001
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ACCESSION   AX059978
VERSION     AX059978.1  GI:12405636
KEYWORDS    .
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9495)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
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            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 96 28-DEC-2000;
            Aventis Pharma S.A. (FR)
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RESULT 15
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DEFINITION  Sequence 91 from Patent WO0078970.
ACCESSION   AX059973
VERSION     AX059973.1  GI:12405631
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SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 91 28-DEC-2000;
            Aventis Pharma S.A. (FR)
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  Best Local Similarity   99.6%;  Pred. No. 8.7e-137;
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Searched: 2185239 seqs, 1125999159 residues

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SUMMARIES

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4	501	100.0	7861	21	AAC69387	Human ABC1 cholest
5	501	100.0	7864	21	AAC69120	Human ABC1 cholest
6	501	100.0	7864	21	AAC69385	Human ABC1 cholest
7	501	100.0	7864	21	AAC69386	Human ABC1 cholest
8	501	100.0	7864	21	AAC69389	Human ABC1 cholest
9	501	100.0	10442	22	AAF24680	Nucleotide sequenc
10	501	100.0	10442	22	AAF24702	Nucleotide sequenc
11	501	100.0	10474	22	AAF24685	Nucleotide sequenc
12	501	100.0	10474	22	AAF24686	Nucleotide sequenc
13	501	100.0	10474	22	AAF24707	Nucleotide sequenc
14	501	100.0	10474	22	AAF24708	Nucleotide sequenc
15	497.8	99.4	6880	21	AAZ94734	Human ATP binding
16	497.8	99.4	6880	22	AAD21325	Human ATP binding
17	497.8	99.4	6880	22	AAI70314	Human ATP binding
18	497.8	99.4	7086	22	ABA09200	Human ABCA1 homolo
19	497.8	99.4	7086	22	AAK52667	Human polynucleoti
20	497.8	99.4	7260	22	AAD21326	Human ATP binding
21	497.8	99.4	7260	22	AAI70315	Human ATP binding
22	497.8	99.4	7281	22	AAK51683	Human polynucleoti
23	497.8	99.4	9741	22	AAS06120	Human ABC1 DNA seq
24	497.8	99.4	9741	24	AAD37273	Human ABC1 full-le
25	497.8	99.4	9854	22	AAS06121	Human ABC1 DNA seq
26	173	34.5	6289	21	AAC69144	Human ABC1 gene ex
27	173	34.5	183999	22	AAF92831	Human ABC1 genomic
28	163.4	32.6	7323	21	AAZ94746	Human ATP binding
29	163.4	32.6	7784	19	AAV33392	ATP binding casset
30	142	28.3	399	22	AAI81212	Human polynucleoti
31	139.4	27.8	5669	22	AAS08707	Human PD-ATP-bindi
32	139.4	27.8	6522	22	AAS08706	Human PD-ATP-bindi
33	137.8	27.5	2911	21	AAZ94751	Human ATP binding
34	137.8	27.5	3437	23	AAS73965	DNA encoding novel
35	137.8	27.5	3635	22	AAF56389	ABC transport rela
36	137.8	27.5	4413	23	AAS83715	DNA encoding novel
c 37	137.8	27.5	5811	22	AAD05626	Human secreted pro
38	137.8	27.5	6768	24	AAS19207	DNA encoding human
39	137.8	27.5	7795	24	ABL57810	Human ABCA7 coding
40	136.2	27.2	6791	24	AAL44693	Human transporter
41	132.4	26.4	5762	22	AAF54792	Nucleotide sequenc
42	132.4	26.4	6607	22	AAF54812	Nucleotide sequenc
43	98.2	19.6	2841	21	AAC69142	Human ABC1 gene ex
44	82	16.4	669	22	AAH08356	Human cDNA clone (
45	82	16.4	5097	22	AAI93913	Human stomach canc

ALIGNMENTS

RESULT 1
AAC69388
ID AAC69388 standard; cDNA; 7857 BP.
XX
AC AAC69388;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX

```
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
DR   P-PSDB; AAB38107.
XX
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Examples; Page -; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
CC   disease, particularly coronary artery disease, but also cerebrovascular
CC   disease, coronary restenosis, and peripheral vascular disease.
CC   Conversely, a high level of HDL has protective effects against
CC   cardiovascular disease. The invention provides genetic constructs and
CC   transgenic cells and non-human animals comprising human ABC1 nucleic
CC   acids, and methods of gene therapy for the treatment or prevention of
CC   cardiovascular disease comprising the administration of an expression
CC   vector encoding ABC1 or an active fragment thereof. The invention also
CC   encompasses compounds which mimic ABC1 activity, compounds which
CC   stimulate ABC1 expression and methods of screening for such compounds.
CC   It further relates to methods for determining whether a patient has an
CC   increased risk for cardiovascular disease due to polymorphisms in the
CC   ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC   or prevent cardiovascular disease, especially coronary artery disease,
CC   cerebrovascular disease, coronary restenosis or peripheral vascular
CC   disease. They may also be used in the treatment of diseases associated
CC   with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC   disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC   present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC   transporter associated with an altered cholesterol level and therefore an
CC   altered risk of cardiovascular disease.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ   Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 21;  Length 7857;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4537 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4596

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4656

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4657 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4716

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4717 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4776

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4836

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4837 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4896

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4897 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4956

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4957 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5016

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5017 CTCTGATGACCACATCAGTGG 5037


RESULT 2
AAF83826
ID   AAF83826 standard; DNA; 7860 BP.
XX
AC   AAF83826;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human ABC1 nucleotide sequence.
XX
KW   ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
KW   LDL; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..3341
FT                   /*tag=  a
FT                   /product= "partial ABC1 protein"
FT                   /note= "the coding sequence continues beyond nucleotide
FT                           3341, possibly till position 6860 as identified
FT                           by translating the present sequence; part of the
FT                           corresponding protein is missing and nucleotide
FT                           3341 corresponds to the last amino acid residue
FT                           (position 1089) as indicated in the
FT                           specification"
XX
PN   WO200132184-A2.
XX
PD   10-MAY-2001.
XX
PF   01-NOV-2000; 2000WO-US30109.
XX
PR   01-NOV-1999;   99US-0162803.
PR   30-JUN-2000; 2000US-0215564.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Attie AD,  Cook M,  Gray-Keller MP,  Hayden MR,  Pimstone S;
PI   Brooks-Wilson A;
XX
DR   WPI; 2001-335779/35.
DR   P-PSDB; AAB62691.
XX
PT   New method for inhibiting cholesterol uptake in the gut comprises
PT   administration of an inhibitor of an ABC1 protein  -
XX
PS   Disclosure; Page 34-36; 41pp; English.
XX
CC   The invention relates to a new method for inhibiting cholesterol uptake
```

CC in the gut that comprises administration of an inhibitor of an ABC1
CC protein. The method is useful for: lowering levels of LDL (low density
CC lipoprotein) cholesterol by reducing the activity of ABC1 protein in the
CC intestinal cells and the abundance of the ABC1 protein in the individual
CC by inhibiting the activity of the protein; identifying drugs that can
CC lower serum cholesterol and LDL levels comprises assaying the drug to
CC test if it can bind to an ABC1 protein; testing LDL cholesterol lowering
CC agents; and for modulation of ABC1 biological activity. The present
CC sequence represents a human ABC1 nucleotide sequence.
XX
SQ Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;

Query Match 100.0%; Score 501; DB 22; Length 7860;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4534 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4593

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4594 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4653

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4654 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4713

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4714 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4773

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4774 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4833

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4834 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4893

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4894 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4953

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4954 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5013

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   5014 CTCTGATGACCACATCAGTGG 5034
```

RESULT 3
AAF92835
ID AAF92835 standard; DNA; 7860 BP.
XX
AC AAF92835;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 cDNA.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-IB01492.
XX
PR 01-SEP-1999; 99US-0151977.
PR 15-MAR-2000; 2000US-0526193.
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
DR WPI; 2001-244356/25.
XX
PT Treating a lower than normal high density lipoprotein-cholesterol
PT (HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity -
XX
PS Disclosure; Fig 2; 317pp; English.
XX
CC The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
SQ Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;

Query Match 100.0%; Score 501; DB 22; Length 7860;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4534 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4593

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4594 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4653

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4654 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4713

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4714 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4773

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4774 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4833

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4834 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4893

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4894 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4953

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4954 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5013

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   5014 CTCTGATGACCACATCAGTGG 5034
```

RESULT 4

```
AAC69387
ID   AAC69387 standard; cDNA; 7861 BP.
XX
AC   AAC69387;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 cholesterol transporter FHA-1 mutant cDNA (delta 2151-2153).
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;   99US-0124702.
PR   08-JUN-1999;   99US-0138048.
PR   17-JUN-1999;   99US-0139600.
PR   01-SEP-1999;   99US-0151977.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
DR   P-PSDB; AAB38106.
XX
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Examples; Page -; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
CC   disease, particularly coronary artery disease, but also cerebrovascular
CC   disease, coronary restenosis, and peripheral vascular disease.
CC   Conversely, a high level of HDL has protective effects against
CC   cardiovascular disease. The invention provides genetic constructs and
CC   transgenic cells and non-human animals comprising human ABC1 nucleic
CC   acids, and methods of gene therapy for the treatment or prevention of
CC   cardiovascular disease comprising the administration of an expression
CC   vector encoding ABC1 or an active fragment thereof. The invention also
CC   encompasses compounds which mimic ABC1 activity, compounds which
CC   stimulate ABC1 expression and methods of screening for such compounds.
CC   It further relates to methods for determining whether a patient has an
CC   increased risk for cardiovascular disease due to polymorphisms in the
CC   ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC   or prevent cardiovascular disease, especially coronary artery disease,
CC   cerebrovascular disease, coronary restenosis or peripheral vascular
CC   disease. They may also be used in the treatment of diseases associated
CC   with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC   disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC   present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC   transporter associated with an altered cholesterol level and therefore an
CC   altered risk of cardiovascular disease.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ   Sequence 7861 BP; 2014 A; 1859 C; 2011 G; 1976 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 21;  Length 7861;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4534 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4593

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4594 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4653

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4654 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4713

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4714 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4773

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4774 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4833

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4834 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4893

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4894 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4953

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4954 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5013

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5014 CTCTGATGACCACATCAGTGG 5034


RESULT 5
AAC69120
ID   AAC69120 standard; cDNA; 7864 BP.
XX
AC   AAC69120;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 cholesterol transporter cDNA.
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200055318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;   99US-0124702.
PR   08-JUN-1999;   99US-0138048.
PR   17-JUN-1999;   99US-0139600.
PR   01-SEP-1999;   99US-0151977.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
DR   P-PSDB; AAB38082.
XX
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Claim 13; Page 157-160; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
CC   disease, particularly coronary artery disease, but also cerebrovascular
CC   disease, coronary restenosis, and peripheral vascular disease.
CC   Conversely, a high level of HDL has protective effects against
CC   cardiovascular disease. The invention provides genetic constructs and
CC   transgenic cells and non-human animals comprising human ABC1 nucleic
CC   acids, and methods of gene therapy for the treatment or prevention of
CC   cardiovascular disease comprising the administration of an expression
CC   vector encoding ABC1 or an active fragment thereof. The invention also
CC   encompasses compounds which mimic ABC1 activity, compounds which
CC   stimulate ABC1 expression and methods of screening for such compounds.
CC   It further relates to methods for determining whether a patient has an
CC   increased risk for cardiovascular disease due to polymorphisms in the
CC   ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC   or prevent cardiovascular disease, especially coronary artery disease,
CC   cerebrovascular disease, coronary restenosis or peripheral vascular
CC   disease. They may also be used in the treatment of diseases associated
CC   with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC   disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC   present sequence represents cDNA encoding the human ABC1 cholesterol
CC   transporter.
XX
SQ   Sequence 7864 BP; 2014 A; 1860 C; 2011 G; 1978 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 21;  Length 7864;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4537 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4596

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4656

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4657 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4716

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4717 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4776

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4836

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4837 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4896

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4897 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4956

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4957 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5016

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5017 CTCTGATGACCACATCAGTGG 5037


RESULT 6
AAC69385
ID   AAC69385 standard; cDNA; 7864 BP.
XX
AC   AAC69385;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;   99US-0124702.
PR   08-JUN-1999;   99US-0138048.
PR   17-JUN-1999;   99US-0139600.
PR   01-SEP-1999;   99US-0151977.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
DR   P-PSDB; AAB38104.
XX
```

```
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Examples; Page -; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
CC   disease, particularly coronary artery disease, but also cerebrovascular
CC   disease, coronary restenosis, and peripheral vascular disease.
CC   Conversely, a high level of HDL has protective effects against
CC   cardiovascular disease. The invention provides genetic constructs and
CC   transgenic cells and non-human animals comprising human ABC1 nucleic
CC   acids, and methods of gene therapy for the treatment or prevention of
CC   cardiovascular disease comprising the administration of an expression
CC   vector encoding ABC1 or an active fragment thereof. The invention also
CC   encompasses compounds which mimic ABC1 activity, compounds which
CC   stimulate ABC1 expression and methods of screening for such compounds.
CC   It further relates to methods for determining whether a patient has an
CC   increased risk for cardiovascular disease due to polymorphisms in the
CC   ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC   or prevent cardiovascular disease, especially coronary artery disease,
CC   cerebrovascular disease, coronary restenosis or peripheral vascular
CC   disease. They may also be used in the treatment of diseases associated
CC   with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC   disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC   present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC   transporter associated with an altered cholesterol level and therefore an
CC   altered risk of cardiovascular disease.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ   Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 21;  Length 7864;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4537 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4596

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4656

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4657 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4716

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4717 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4776

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4836

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4837 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4896

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4897 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4956

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4957 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5016

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5017 CTCTGATGACCACATCAGTGG 5037


RESULT 7
AAC69386
ID   AAC69386 standard; cDNA; 7864 BP.
XX
AC   AAC69386;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864G).
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;   99US-0124702.
PR   08-JUN-1999;   99US-0138048.
PR   17-JUN-1999;   99US-0139600.
PR   01-SEP-1999;   99US-0151977.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
DR   P-PSDB; AAB38105.
XX
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Examples; Page -; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
```

CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC transporter associated with an altered cholesterol level and therefore an
CC altered risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ Sequence 7864 BP; 2013 A; 1860 C; 2012 G; 1978 T; 1 other;

Query Match 100.0%; Score 501; DB 21; Length 7864;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
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Db    4537 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4596

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4656

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4657 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4716

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4717 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4776

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4836

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4837 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4896

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4897 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4956

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4957 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5016

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5017 CTCTGATGACCACATCAGTGG 5037
```

RESULT 8
AAC69389
ID AAC69389 standard; cDNA; 7864 BP.
XX
AC AAC69389;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 cholesterol transporter FHA-2 mutant cDNA (C6504T).
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX
DR WPI; 2000-587528/55.
DR P-PSDB; AAB38108.
XX
PT New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT disease and cancer -
XX
PS Examples; Page -; 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

```
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC   present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC   transporter associated with an altered cholesterol level and therefore an
CC   altered risk of cardiovascular disease.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ   Sequence 7864 BP; 2014 A; 1859 C; 2011 G; 1979 T; 1 other;

  Query Match            100.0%;  Score 501;  DB 21;  Length 7864;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4537 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4596

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4656

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4657 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4716

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4717 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4776

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db    4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4836

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    4837 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4896

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4897 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4956

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4957 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5016

Qy     481 CTCTGATGACCACATCAGTGG 501
          ||||||||||||||||||||
Db    5017 CTCTGATGACCACATCAGTGG 5037


RESULT 9
AAF24680
ID   AAF24680 standard; DNA; 10442 BP.
XX
AC   AAF24680;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of a human ABC1 polypeptide.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             291..7076
FT                   /*tag= a
FT                   /product= "ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 122-128; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC   membranes and utilises ATP hydrolysis to transport a wide variety of
CC   substrates across the plasma membrane. ABC1 is a pivotal protein in
CC   the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC   stores. ABC1 is defective in Tangier disease, a genetic disorder
CC   characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC   localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC   useful for developing pharmaceutical agents for the treatment of heart
CC   disease and other disorders associated with hypercholesterolemia and
CC   atherosclerosis. The genes are useful for developing screening assays to
CC   screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   are also useful as diagnostic indicators of cardiovascular disease and
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

  Query Match            100.0%;  Score 501;  DB 22;  Length 10442;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4750 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4809

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4810 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4869

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4870 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4929

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4930 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4989

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4990 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5049

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5050 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5109

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5110 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5169
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Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5170 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5229

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   5230 CTCTGATGACCACATCAGTGG 5250
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RESULT 10
AAF24702
ID AAF24702 standard; DNA; 10442 BP.
XX
AC AAF24702;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
DR P-PSDB; AAB31365.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Claim 3; Page 117-123; 211pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX

SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 8.2e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4750 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4809

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4810 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4869

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4870 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4929

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4930 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4989

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4990 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5049

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5050 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5109

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5110 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5169

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5170 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5229

Qy    481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db   5230 CTCTGATGACCACATCAGTGG 5250
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RESULT 11
AAF24685
ID AAF24685 standard; DNA; 10474 BP.
XX
AC AAF24685;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 323..7108
FT /*tag= a
FT /product= "defective ABC1 polypeptide"
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.

```
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 148-154; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy     481 CTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||
Db    5262 CTCTGATGACCACATCAGTGG 5282
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RESULT 12
AAF24686
ID   AAF24686 standard; DNA; 10474 BP.
XX
AC   AAF24686;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 170-176; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841
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Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db    4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy     481 CTCTGATGACCACATCAGTGG 501
           |||||||||||||||||||||
Db    5262 CTCTGATGACCACATCAGTGG 5282
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RESULT 13
AAF24707
ID AAF24707 standard; DNA; 10474 BP.
XX
AC AAF24707;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 323..7108
FT /*tag= a
FT /product= "defective ABC1 polypeptide"
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
DR P-PSDB; AAB31366.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Claim 27; Page 144-150; 211pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
XX
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 8.2e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy     481 CTCTGATGACCACATCAGTGG 501
           |||||||||||||||||||||
Db    5262 CTCTGATGACCACATCAGTGG 5282
```

RESULT 14
AAF24708
ID AAF24708 standard; DNA; 10474 BP.
XX
AC AAF24708;

```
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag= a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31367.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 30; Page 165-172; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-148;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4782 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4841

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4842 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4901

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4902 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4961

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4962 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5021

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5022 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5081

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5082 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5141

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5142 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5201

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db    5202 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5261

Qy     481 CTCTGATGACCACATCAGTGG 501
           |||||||||||||||||||||
Db    5262 CTCTGATGACCACATCAGTGG 5282


RESULT 15
AAZ94734
ID   AAZ94734 standard; cDNA; 6880 BP.
XX
AC   AAZ94734;
XX
DT   01-AUG-2000  (first entry)
XX
DE   Human ATP binding cassette ABCA1 (ABC1) cDNA.
XX
KW   ABCA1; ABC1; ATP binding cassette; human; cholesterol;
KW   interleukin-1 beta; transporter; inflammation; septic shock;
KW   rheumatoid arthritis; Tangier disease; hypertriglyceridemia;
KW   splenomegaly; atherosclerosis; lipid disorder; dyslipidemia;
KW   psoriasis; lupus erythematosus; diagnosis; gene therapy;
KW   chromosome 9q22-31; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             121..6726
FT                   /*tag= a
XX
PN   WO200018912-A2.
XX
PD   06-APR-2000.
XX
PF   21-SEP-1999;   99WO-EP06991.
XX
PR   25-SEP-1998;   98US-0101706.
XX
PA   (FARB ) BAYER AG.
XX
PI   Schmitz G,  Klucken J;
XX
DR   WPI; 2000-293151/25.
DR   P-PSDB; AAY79380.
XX
PT   Adenosine triphosphate binding proteins useful for identifying agents
PT   for treating atherosclerosis and other inflammatory disorders -
XX
PS   Claim 9; Page 90-93; 154pp; English.
XX
CC   The present sequence is that of human cDNA encoding ATP binding
```

```
CC   cassette protein ABCA1 (ABC1, see AAY79380), the human homologue of
CC   mouse ABCA1.  The cDNA was identified using a differential display
CC   method in which monocytes from peripheral blood were subjected to
CC   macrophage differentiation and cholesterol loading with acetylated
CC   low density lipoproteins and subsequent deloading with high density
CC   lipoprotein (HDL3) to identify cholesterol sensitive genes.  The
CC   ABCA1 gene maps to human chromosome 9q22-31.  Dysregulated ABCA1
CC   is the gene locus involved in the HDL deficiency syndrome
CC   Tangier disease, associated with hypertriglyceridemia and
CC   splenomegaly.  ABCA1 is also a transporter for interleukin-1 beta,
CC   making the gene a candidate for treatment of inflammatory diseases
CC   such as rheumatoid arthritis and septic shock.  The invention
CC   also provides other cholesterol-sensitive ABC genes (see AAZ94735-63)
CC   that can be used for diagnostic and therapeutic applications,
CC   and for biochemical or cell-based assays to screen for
CC   pharmacologically active compounds useful for the treatment of
CC   lipid disorders, atherosclerosis or other inflammatory diseases
CC   such as psoriasis and lupus erythematosus.
XX
SQ   Sequence 6880 BP; 1760 A; 1656 C; 1783 G; 1681 T; 0 other;

  Query Match             99.4%;  Score 497.8;  DB 21;  Length 6880;
  Best Local Similarity   99.6%;  Pred. No. 6.9e-147;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4400 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4459

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db    4460 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4519

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
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Db    4520 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4579

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db    4580 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4639

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4640 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4699

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4700 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4759

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Db    4760 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4819

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    4880 CTCCGATGACCACATCAGTGG 4900


Search completed: April  3, 2003, 13:37:16
Job time : 130.452 secs
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Run on: April 3, 2003, 09:40:44 ; Search time 13.777 Seconds
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Title: US-09-595-526C-1_COPY_4750_5250
Perfect score: 501
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	39.4	7.9	7218	1	US-08-232-463-14	Sequence 14, Appl
c	2	33.2	6.6	162450	4	US-09-345-882-1	Sequence 1, Appli
	3	31.6	6.3	5679	1	US-08-201-697-1	Sequence 1, Appli
	4	30.8	6.1	1951	1	US-08-487-890A-112	Sequence 112, App
	5	30.8	6.1	1951	2	US-08-478-435-112	Sequence 112, App
	6	30.8	6.1	1951	2	US-08-337-483-112	Sequence 112, App
	7	30.8	6.1	1951	2	US-08-478-373-112	Sequence 112, App
	8	30.8	6.1	1951	3	US-08-474-671-112	Sequence 112, App
	9	30.8	6.1	1951	3	US-08-483-577A-112	Sequence 112, App
	10	30.8	6.1	1951	4	US-08-897-438-112	Sequence 112, App
	11	30.8	6.1	1951	4	US-08-637-654-112	Sequence 112, App
	12	30.8	6.1	1951	4	US-08-649-518-112	Sequence 112, App
	13	30.6	6.1	315	3	US-09-157-177-104	Sequence 104, App
c	14	30.6	6.1	2834	1	US-08-276-151-8	Sequence 8, Appli
c	15	30.6	6.1	3073	1	US-07-688-352C-31	Sequence 31, Appl
c	16	30.6	6.1	3073	2	US-08-474-379C-31	Sequence 31, Appl
c	17	30.6	6.1	3073	3	US-09-146-249A-31	Sequence 31, Appl
c	18	30.6	6.1	3073	3	US-08-206-188B-31	Sequence 31, Appl
c	19	30.6	6.1	3073	5	PCT-US91-02714-30	Sequence 30, Appl
	20	30.6	6.1	35100	1	US-08-306-691B-19	Sequence 19, Appl
	21	30.6	6.1	35100	5	PCT-US93-06251-19	Sequence 19, Appl
	22	30.4	6.1	2166	4	US-09-134-078-5	Sequence 5, Appli
c	23	30.2	6.0	98844	4	US-09-791-211-10	Sequence 10, Appl
	24	29.8	5.9	2026	2	US-08-993-228-3	Sequence 3, Appli
	25	29.6	5.9	2618	4	US-09-488-671-17	Sequence 17, Appl
	26	29.4	5.9	3889	4	US-09-484-970B-39	Sequence 39, Appl
	27	29.2	5.8	1866	1	US-08-403-388-1	Sequence 1, Appli
	28	29.2	5.8	1866	1	US-08-658-578-1	Sequence 1, Appli
	29	29.2	5.8	1866	3	US-08-846-111D-1	Sequence 1, Appli
	30	29.2	5.8	1866	4	US-09-056-105-19	Sequence 19, Appl
	31	29.2	5.8	1866	4	US-09-443-077-1	Sequence 1, Appli
	32	29.2	5.8	5099	1	US-08-487-890A-4	Sequence 4, Appli
	33	29.2	5.8	5099	2	US-08-478-435-4	Sequence 4, Appli
	34	29.2	5.8	5099	2	US-08-337-483-4	Sequence 4, Appli
	35	29.2	5.8	5099	2	US-08-478-373-4	Sequence 4, Appli
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	37	29.2	5.8	5099	3	US-08-483-577A-4	Sequence 4, Appli
	38	29.2	5.8	5099	4	US-08-897-438-4	Sequence 4, Appli
	39	29.2	5.8	5099	4	US-08-637-654-4	Sequence 4, Appli
	40	29.2	5.8	5099	4	US-08-649-518-4	Sequence 4, Appli
	41	29.2	5.8	40352	3	US-08-846-111D-15	Sequence 15, Appl
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c	44	29	5.8	2176	3	US-09-090-808-3	Sequence 3, Appli
c	45	29	5.8	2176	4	US-09-447-453-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 7.9%; Score 39.4; DB 1; Length 7218;

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  Best Local Similarity   5.7%;  Pred. No. 0.012;
  Matches   22;  Conservative  196;  Mismatches  167;  Indels    0;  Gaps    0;

Qy       4 AAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGGATT 63
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Qy      64 ATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGA 123
           :   :: ::::: : : : : :::  : ::  :::::   :::::: ::::   ::: ::
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Qy     124 ATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGA 183
           : :::   ::: : :: ::          ::: :  :: :: :   ::: :         ::
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Qy     184 GTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACA 243
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Qy     244 GTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAA 303
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Qy     364 TCATCAACAATGCCATTCTCCGGGC 388
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Db    1041 CAAGCTCGGAATTAATTCTGTGAGC 1017


RESULT 2
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: GENSET.031A
;  CURRENT APPLICATION NUMBER: US/09/345,882
;  CURRENT FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 1
;   LENGTH: 162450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 72794
;   OTHER INFORMATION: 5-124-273  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 88073
;   OTHER INFORMATION: 5-127-261  :  polymorphic  base  A  or  C
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 90842
;   OTHER INFORMATION: 99-1437-325  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 93714
;   OTHER INFORMATION: 5-128-60  :  polymorphic  base  deletion  of  GT
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97122
;   OTHER INFORMATION: 99-1442-224  :  polymorphic  base  G  or  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97152
;   OTHER INFORMATION: 5-129-144  :  polymorphic  base  deletion  of  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99098
;   OTHER INFORMATION: 5-130-257  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99117
;   OTHER INFORMATION: 5-130-276  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 103806
;   OTHER INFORMATION: 5-131-395  :  polymorphic  base  A  or  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 106940
;   OTHER INFORMATION: 5-133-375  :  polymorphic  base  insertion  of  A
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108106
;   OTHER INFORMATION: 5-135-155  :  polymorphic  base  insertion  of  A
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108149
;   OTHER INFORMATION: 5-135-198  :  polymorphic  base  insertion  of  GTTT
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108308
;   OTHER INFORMATION: 5-135-357  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108471
;   OTHER INFORMATION: 5-136-174  :  polymorphic  base  C  or  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 134134
;   OTHER INFORMATION: 5-140-120  :  polymorphic  base  C  or  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 134362
;   OTHER INFORMATION: 5-140-348  :  polymorphic  base  insertion  of  A
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 134374
;   OTHER INFORMATION: 5-140-361  :  polymorphic  base  insertion  of  CA
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 146328
;   OTHER INFORMATION: 5-143-84  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 146345
;   OTHER INFORMATION: 5-143-101  :  polymorphic  base  A  or  C
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 150329
;   OTHER INFORMATION: 5-145-24  :  polymorphic  base  A  or  G
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 160031
;   OTHER INFORMATION: 5-148-352  :  polymorphic  base  G  or  T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 72771..72817
;   OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 72771..72817
;   OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
;   FEATURE:
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;   NAME/KEY: allele
;   LOCATION: 88050..88096
;   OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 88050..88096
;   OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 90819..90865
;   OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 90819..90865
;   OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 93690..93736
;   OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 93690..93736
;   OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97099..97145
;   OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97099..97145
;   OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97130..97177
;   OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 97130..97177
;   OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99075..99121
;   OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99075..99121
;   OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99094..99140
;   OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 99094..99140
;   OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 103783..103828
;   OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 103783..103828
;   OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 106918..106966
;   OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 106918..106966
;   OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108084..108130
;   OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108084..108130
;   OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108127..108177
;   OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 108127..108177
;   OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
;   FEATURE:

  Query Match             6.6%;  Score 33.2;  DB 4;  Length 162450;
  Best Local Similarity   51.3%;  Pred. No. 7.2;
  Matches   77;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy     235 CCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGG 294
           | ||| | ||      ||| ||   |  ||| ||  |||| | | ||  |    |   |
Db   41002 CAAAGAAAAGAGAACTAGAGAGACACCCAAACTGCAGGGGAGGTTGTAGTAACAAAGCAG 40943

Qy     295 ACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTT 354
           |   || ||  ||  || ||||| || |  |   ||||  | | |       |  | |||
Db   40942 AAGACAAAAGGAAATTCCAGGTGAGGCTACAGGGCAAGAACAGTCTCATTGTGTGTTCTG 40883

Qy     355 TCCTGAATGTCATCAACAATGCCATTCTCC 384
           || |||||||     | | | ||| | | |
Db   40882 TCTTGAATGTACCAGAAACTACCAGTGTTC 40853


RESULT 3
US-08-201-697-1
; Sequence 1, Application US/08201697
; Patent No. 5705623
; GENERAL INFORMATION:
;   APPLICANT:  Wiggins, Roger C.
;   APPLICANT:  Thomas, Peedikayil E.
;   TITLE OF INVENTION:  Mammalian Glomerular Epithelial Protein
;   TITLE OF INVENTION:  1
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Campbell and Flores
;     STREET:  4370 La Jolla Village Drive, Suite 700
;     CITY:  San Diego
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  92122
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/201,697
;     FILING DATE:  25-FEB-1994
;     CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Campbell, Cathryb A.
;     REGISTRATION NUMBER:  31,815
;     REFERENCE/DOCKET NUMBER:  P-UM 9783
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (619) 535-9001
;     TELEFAX:  (619) 535-8949
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  5679 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   FEATURE:
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;      NAME/KEY:  CDS
;      LOCATION:  180..3740
US-08-201-697-1

  Query Match             6.3%;  Score 31.6;  DB 1;  Length 5679;
  Best Local Similarity   58.5%;  Pred. No. 3.8;
  Matches   55;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy     172 CACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGC 231
           ||||||      |||       ||  |  |  |||||  |  | ||||||||| ||  ||
Db    2668 CACTTCTAATTGGTCTGCTGCTTGTTACTCTCATCATTCTTAGGAAGAAACATCTGCAGA 2727

Qy     232 TGGCCAAGGACAGTTCTGCAGATCGATTTCTCAA 265
           ||||  |  |||  ||   ||||    |||| ||||
Db    2728 TGGCTAGGGAGTGTGGAGCAGGAACATTTGTCAA 2761


RESULT 4
US-08-487-890A-112
; Sequence 112, Application US/08487890A
; Patent No. 5708149
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor, 330 Unviersity Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,890A
;      FILING DATE:  07-JUN-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-466 MIS:jb
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-487-890A-112

  Query Match             6.1%;  Score 30.8;  DB 1;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||      | ||| | | | |       |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           |||||  |||  |       | | ||||  |||||  |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 5
US-08-478-435-112
; Sequence 112, Application US/08478435
; Patent No. 5922323
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  Suite 701, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,435
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-462 MIS:vg
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-478-435-112

  Query Match             6.1%;  Score 30.8;  DB 2;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
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  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |      |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           ||||| ||| |      | | ||||  ||||| |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 6
US-08-337-483-112
; Sequence 112, Application US/08337483
; Patent No. 5922562
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  Suite 701, 330 Unviersity Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/337,483
;      FILING DATE:  08-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-410 MIS:jb
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-337-483-112

  Query Match             6.1%;  Score 30.8;  DB 2;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |      |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           ||||| ||| |      | | ||||  ||||| |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 7
US-08-478-373-112
; Sequence 112, Application US/08478373
; Patent No. 5922841
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  Suite 701, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,373
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-463 MIS:vg
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-478-373-112

  Query Match             6.1%;  Score 30.8;  DB 2;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |      |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           ||||| ||| |      | | ||||  ||||| |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 8
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US-08-474-671-112
; Sequence 112, Application US/08474671
; Patent No. 6008326
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  Suite 701, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,671
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-465 MIS:vg
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-474-671-112

  Query Match             6.1%;  Score 30.8;  DB 3;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy    183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
          | || ||||| | |||     | ||| | | | |      | ||||||   |||| ||
Db    790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy    243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
            ||||| ||| |      | | ||||  ||||| |||
Db    850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 9
US-08-483-577A-112
; Sequence 112, Application US/08483577A
; Patent No. 6015688
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  160
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  Suite 701, 330 Unviersity Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,577A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-511
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-483-577A-112

  Query Match             6.1%;  Score 30.8;  DB 3;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

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Db    790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy    243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
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Db    850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 10
US-08-897-438-112
; Sequence 112, Application US/08897438
; Patent No. 6262016
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;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  160
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/897,438
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/483,577
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-720
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-897-438-112

  Query Match             6.1%;  Score 30.8;  DB 4;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |      |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           |||||  |||  |      | |  ||||  |||||  |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 11
US-08-637-654-112
; Sequence 112, Application US/08637654
; Patent No. 6358727
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena M
;    APPLICANT:  Harkness, Robin E
;    APPLICANT:  Schryvers, Anthony B
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
;    APPLICANT:  Murdin, Andrew D
;    APPLICANT:  Klein, Michel H
;    TITLE OF INVENTION:  HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/637,654
;      FILING DATE:  05-AUG-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/CA94/00616
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-595
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-637-654-112

  Query Match             6.1%;  Score 30.8;  DB 4;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |      |  ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           |||||  |||  |      | |  ||||  |||||  |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 12
US-08-649-518-112
; Sequence 112, Application US/08649518
; Patent No. 6361779
;  GENERAL INFORMATION:
;    APPLICANT:  Loosmore, Sheena
;    APPLICANT:  Harkness, Robin
;    APPLICANT:  Schryvers, Anthony
;    APPLICANT:  Chong, Pele
;    APPLICANT:  Gray-Owen, Scott
;    APPLICANT:  Yang, Yan-Ping
```

```
;    APPLICANT:  Murdin, Andrew
;    APPLICANT:  Klein, Michel
;    TITLE OF INVENTION:  Transferrin Receptor Genes
;    NUMBER OF SEQUENCES:  160
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor, 330 Unviersity Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/649,518
;      FILING DATE:  17-MAY-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/337,483
;      FILING DATE:  08-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/483,577
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,116
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/148,968
;      FILING DATE:  08-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1890
US-08-649-518-112

  Query Match             6.1%;  Score 30.8;  DB 4;  Length 1951;
  Best Local Similarity   57.1%;  Pred. No. 3.8;
  Matches   56;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy     183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
           | || ||||| | |||     | ||| | | | |     | ||||||   |||| ||
Db     790 AATCTAGAAGCTGATGTGTATAGCAACCGATTCAGAGGTAAAGTAAAGCCAACCAAAGAG 849

Qy     243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
           |||||  ||| |      | | ||||  |||||  |||
Db     850 TCTTCTGAAGAACATCCCTTTACCAGCGAGGGAACATT 887


RESULT 13
US-09-157-177-104
; Sequence 104, Application US/09157177
; Patent No. 6090558
; GENERAL INFORMATION:
;  APPLICANT: Butler, John M.
;  APPLICANT: Li, Jia
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT: Becker, Christopher H.
;  TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY WITH  POLYMORPHIC DNA
;  TITLE OF INVENTION: REPEAT MARKERS
;  FILE REFERENCE: GETR:017/GETR017P
;  CURRENT APPLICATION NUMBER: US/09/157,177
;  CURRENT FILING DATE: 1998-09-18
;  EARLIER APPLICATION NUMBER: 60/059,415
;  EARLIER FILING DATE: 1997-09-19
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
;   LENGTH: 315
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-157-177-104

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  Best Local Similarity   60.0%;  Pred. No. 1.6;
  Matches   51;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

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Db     133 GATAGATAGATAGATAGATAGATAGATAGATAGGAAGTACTTAGAACAGGGTCTGACACA 192

Qy     300 AGAAATAATGTCAAGGTGTGGTTCA 324
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Db     193 GGAAATGCTGTCCAAGTGTGCACCA 217


RESULT 14
US-08-276-151-8/c
; Sequence 8, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
;    APPLICANT:  Freed, Ellen
;    APPLICANT:  Ruggieri, Rosamaria
;    TITLE OF INVENTION:  Interaction of raf-1 and 14-3-3 Proteins
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward et al.
;      STREET:  Five Palo ALto Square
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,151
;      FILING DATE:  14-JUL-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Ph.D., Timothy E
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  ONYX-005/00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 843-5481
;      TELEFAX:  (415) 857-0663
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  85..822
US-08-276-151-8
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Query Match 6.1%; Score 30.6; DB 1; Length 2834;
Best Local Similarity 53.8%; Pred. No. 5.4;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Db    2327 AGACAGAAGGCTAAAACAGGAAGGTAATCTTGTGCACCTGACAAATAGAAAGAATAAAGG 2268

Qy      62 TTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTG 118
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RESULT 15
US-07-688-352C-31/c
; Sequence 31, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3073 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1111
US-07-688-352C-31

Query Match 6.1%; Score 30.6; DB 1; Length 3073;
Best Local Similarity 53.8%; Pred. No. 5.7;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Qy      62 TTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTG 118
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Title: US-09-595-526C-1_COPY_4750_5250
Perfect score: 501
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	497.8	99.4	8925	9	US-09-802-640-27	Sequence 27, Appl
2	497.8	99.4	9741	10	US-09-846-456-10	Sequence 10, Appl
3	497.8	99.4	9870	9	US-09-984-827-92	Sequence 92, Appl
4	497.8	99.4	9870	9	US-09-984-827-93	Sequence 93, Appl
5	497.8	99.4	9870	9	US-09-984-827-94	Sequence 94, Appl
6	497.8	99.4	9870	9	US-09-984-827-95	Sequence 95, Appl
7	497.8	99.4	9870	9	US-09-984-827-96	Sequence 96, Appl
8	497.8	99.4	9870	9	US-09-984-827-97	Sequence 97, Appl
9	497.8	99.4	9870	9	US-09-984-827-98	Sequence 98, Appl
10	497.8	99.4	9870	9	US-09-984-827-99	Sequence 99, Appl
11	497.8	99.4	9870	9	US-09-984-827-100	Sequence 100, App
12	497.8	99.4	9870	9	US-09-984-827-101	Sequence 101, App
13	497.8	99.4	9870	9	US-09-984-827-102	Sequence 102, App
14	497.8	99.4	9870	9	US-09-984-827-103	Sequence 103, App
15	497.8	99.4	9870	9	US-09-984-827-104	Sequence 104, App
16	497.8	99.4	9870	9	US-09-984-827-105	Sequence 105, App
17	497.8	99.4	9870	9	US-09-984-827-106	Sequence 106, App
18	497.8	99.4	9870	9	US-09-984-827-107	Sequence 107, App
19	497.8	99.4	9870	9	US-09-984-827-108	Sequence 108, App
20	497.8	99.4	9870	9	US-09-984-827-109	Sequence 109, App
21	497.8	99.4	9870	9	US-09-984-827-110	Sequence 110, App
22	497.8	99.4	9870	9	US-09-984-827-111	Sequence 111, App
23	497.8	99.4	9870	9	US-09-984-827-112	Sequence 112, App
24	497.8	99.4	9870	9	US-09-984-827-113	Sequence 113, App
25	497.8	99.4	9870	9	US-09-984-827-114	Sequence 114, App
26	497.8	99.4	9870	9	US-09-984-827-115	Sequence 115, App
27	497.8	99.4	9870	9	US-09-984-827-116	Sequence 116, App
28	497.8	99.4	9870	9	US-09-984-827-117	Sequence 117, App
29	497.8	99.4	9870	9	US-09-984-827-118	Sequence 118, App
30	497.8	99.4	9870	9	US-09-984-827-119	Sequence 119, App
31	497.8	99.4	9870	9	US-09-984-827-120	Sequence 120, App
32	497.8	99.4	9870	9	US-09-984-827-121	Sequence 121, App
33	497.8	99.4	9870	9	US-09-984-827-122	Sequence 122, App
34	497.8	99.4	9870	9	US-09-984-827-123	Sequence 123, App
35	497.8	99.4	9870	9	US-09-984-827-124	Sequence 124, App
36	497.8	99.4	9870	9	US-09-984-827-125	Sequence 125, App
37	497.8	99.4	9870	9	US-09-984-827-126	Sequence 126, App
38	496.2	99.0	9741	9	US-09-984-827-1	Sequence 1, Appli
39	139.4	27.8	4653	10	US-09-995-542-7	Sequence 7, Appli
40	139.4	27.8	6804	10	US-09-995-542-4	Sequence 4, Appli
41	137.8	27.5	3609	10	US-09-833-381-958	Sequence 958, App
42	137.8	27.5	3635	10	US-09-767-870-3	Sequence 3, Appli
43	137.8	27.5	6432	10	US-09-858-194-3	Sequence 3, Appli
44	137.8	27.5	6768	10	US-09-858-194-1	Sequence 1, Appli
45	132.4	26.4	6633	10	US-09-995-542-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-802-640-27
; Sequence 27, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kleyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 8925
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5020)...(6162)
; OTHER INFORMATION: Nucleotide encoding ATP-binding cassette (ABC1)
; OTHER INFORMATION: n= a or g or c or t
US-09-802-640-27

Query Match 99.4%; Score 497.8; DB 9; Length 8925;
Best Local Similarity 99.6%; Pred. No. 4.6e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4399 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4458

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4459 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4518

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4519 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4578
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Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4579 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4638

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4639 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4698

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4699 AAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4758

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4759 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 4818

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4819 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 4878

Qy     481 CTCTGATGACCACATCAGTGG 501
           ||| ||||||||||||||||||
Db    4879 CTCGGATGACCACATCAGTGG 4899
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RESULT 2
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denefle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: Fojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

Query Match 99.4%; Score 497.8; DB 10; Length 9741;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4644 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4703

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4704 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4763

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4764 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4823
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Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    4824 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 4883

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4884 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4943

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4944 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5003

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5004 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5063

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5064 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5123

Qy     481 CTCTGATGACCACATCAGTGG 501
           ||| ||||||||||||||||||
Db    5124 CTCCGATGACCACATCAGTGG 5144
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RESULT 3
US-09-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-92

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
Db   5253 CTCCGATGACCACATCAGTGG 5273


RESULT 4
US-09-984-827-93
; Sequence 93, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-93

  Query Match            99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity  99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
Db   5253 CTCCGATGACCACATCAGTGG 5273


RESULT 5
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-94

  Query Match            99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity  99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012
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```
Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273
```

RESULT 6
US-09-984-827-95
; Sequence 95, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-95

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012
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```
Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273
```

RESULT 7
US-09-984-827-96
; Sequence 96, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-96

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273


RESULT 8
US-09-984-827-97
; Sequence 97, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-97

  Query Match             99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy    301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273


RESULT 9
US-09-984-827-98
; Sequence 98, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-98

  Query Match             99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy    121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy    181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy    241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072
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Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy     481 CTCTGATGACCACATCAGTGG 501
           ||| ||||||||||||||||||
Db    5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 10
US-09-984-827-99
; Sequence 99, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-99

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072
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Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy     481 CTCTGATGACCACATCAGTGG 501
           ||| ||||||||||||||||||
Db    5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 11
US-09-984-827-100
; Sequence 100, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-100

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 12
US-09-984-827-101
; Sequence 101, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-101

  Query Match             99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy    361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

Qy    421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy    481 CTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||||||
Db   5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 13
US-09-984-827-102
; Sequence 102, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-102

  Query Match             99.4%;  Score 497.8;  DB 9;  Length 9870;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-153;
  Matches  499;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
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Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
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Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132
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Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Db    5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 14
US-09-984-827-103
; Sequence 103, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-103

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132
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Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Qy     421 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 480
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Qy     481 CTCTGATGACCACATCAGTGG 501
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Db    5253 CTCCGATGACCACATCAGTGG 5273
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RESULT 15
US-09-984-827-104
; Sequence 104, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-104

Query Match 99.4%; Score 497.8; DB 9; Length 9870;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4773 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 4832

Qy      61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4833 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGG 4892

Qy     121 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4893 TGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTC 4952

Qy     181 CGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 240
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Db    4953 CGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG 5012

Qy     241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

Qy     301 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360
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Db    5073 GAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132

Qy     361 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 420
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Db   5133 ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATT 5192

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Db   5193 ATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGG 5252

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Db   5253 CTCCGATGACCACATCAGTGG 5273


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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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23: em_gss_mam:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	308.8	61.6	381	12	BE757461	BE757461 211904 MA
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	15	83.8	16.7	426	14	H87069	H87069 ys74d05.r1
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	23	72.2	14.4	946	17	CNS027TF	AL185100 Tetraodon
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	36	53.4	10.7	926	17	CNS03F4P	AL241234 Tetraodon
	37	51.2	10.2	440	12	BF600656	BF600656 265404 MA
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	40	50	10.0	561	13	BG921440	BG921440 602824325
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ALIGNMENTS

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LOCUS BE715104 463 bp mRNA linear EST 12-SEP-2000
DEFINITION MR3-HT0737-060700-004-b09 HT0737 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE715104
VERSION BE715104.1 GI:10103369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

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            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-HT0737-060
            700-004-b09&t3=2000-07-06&t4=1)
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            High quality sequence start: 24
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                     /dev_stage="Adult"
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                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      147 a    105 c    111 g    100 t
ORIGIN

  Query Match             85.6%;  Score 428.8;  DB 12;  Length 463;
  Best Local Similarity   97.3%;  Pred. No. 3.8e-108;
  Matches  436;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      21 GCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGGATTATCTGGTGAAGACGTAT 80
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Qy      81 GTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGC 140
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Qy     141 GGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGAT 200
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Qy     201 GCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTT 260
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Qy     261 CTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGG 320
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Db     246 CTCAACAGCTAGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCGAGGTGTGG 305

Qy     321 TTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATT 380
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Qy     441 CATCCCCTGAATCTCACCAAGCAGCAGC 468
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Db     426 CATCCCCGGAATCTCACCTAGCAGCAGC 453


RESULT 2
BE757461
LOCUS       BE757461                381 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  211904 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE757461
VERSION     BE757461.1  GI:10171453
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 381)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
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            and -minmatch 12 options.
            PCR PRimers
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            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 64  row: N  column: 3
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .381
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT      111 a     92 c     95 g     83 t
ORIGIN

  Query Match             61.6%;  Score 308.8;  DB 12;  Length 381;
  Best Local Similarity   89.9%;  Pred. No. 6.3e-75;
  Matches  331;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy     126 GAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGT 185
           |||||||||| || || |||||||||||| ||||||| |||| ||||||||||||||
Db       1 GAGTTTAGGTACGGTGGATTTTCCCTGGGTGCCAGTAATTCTCAGTCACTTCCTCCGAGT 60

Qy     186 CAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGT 245
           |||||||||||||||||||||| |||||||||||||| | ||| ||| ||||||||||
Db      61 GAAGAAGTTAATGATGCCATCAAGCAAATGAAGAAACACTTGAAGGTGGTCAAGGACAGT 120

Qy     246 TCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAAT 305
           |||||||| |||||||||| |||||||||||| || |||||||||||||||| | ||||
Db     121 TCTGCAGACCGATTTCTCAGCAGCTTGGGAAGGTTCATGACAGGACTGGACACAAAAAAT 180

Qy     306 AATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTC 365
           || |||||||||||||||| |||||||||||||||| |||||||||| ||||||||
Db     181 AACGTCAAGGTGTGGTTCAACAACAAGGGCTGGCATGCCATCAGCTCTTTCTTGAATGTC 240

Qy     366 ATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGA 425
           |||||||||||||||||||||||||| ||||| |||||||||||||| ||||| ||||
Db     241 ATCAACAATGCCATTCTCCGGGCCAATCTGCAGAAGGGAGAGAACCCCAGCCAGTATGGG 300

Qy     426 ATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 485
           |||||||||||||||| || ||||| |||||||||||||||||||| ||| | | | |
Db     301 ATTACTGCTTTCAATCACCCGCTGAACCTCACCAAGCAGCAGCTCTCAGAAGTGACACAG 360

Qy     486 ATGACCAC 493
           ||| |||
Db     361 ATGGACAC 368


RESULT 3
BF855659
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LOCUS       BF855659                 376 bp    mRNA    linear   EST 16-JAN-2001
DEFINITION  RC6-FN0202-171100-012-D01 FN0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF855659
VERSION     BF855659.1  GI:12243403
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6&t2=RC6-FN0202-
            171100-012-D01&t3=2000-11-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 351.
FEATURES             Location/Qualifiers
     source          1..376
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="FN0202"
                     /dev_stage="Adult"
                     /note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
                     ; Site_2: SmaI; A mini-library was made by cloning
                     products derived from  ORESTES PCR (U.S. Letters Patent
                     application No. 196,716 -  Ludwig Institute for Cancer
                     Research) profiles into  the pUC 18 vector. Reverse
                     transcription of tissue mRNA and cDNA amplification were
                     performed under low stringency conditions."
BASE COUNT       85 a     83 c     92 g    115 t      1 others
ORIGIN

  Query Match             34.5%;  Score 173;  DB 12;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-37;
  Matches  173;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 AGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACA 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACA 237

Qy        373 ATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTG 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTG 297

Qy        433 CTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 485
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 350


RESULT 4
BE905243
LOCUS       BE905243                1089 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601499284F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901125 5',
            mRNA sequence.
ACCESSION   BE905243
VERSION     BE905243.1  GI:10398332
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1089)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9701  row: h  column: 22
            High quality sequence stop: 652.
FEATURES             Location/Qualifiers
     source          1..1089
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3901125"
                     /clone_lib="NIH_MGC_70"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      319 a    265 c    286 g    219 t
ORIGIN

  Query Match             32.2%;  Score 161.4;  DB 12;  Length 1089;
  Best Local Similarity   57.7%;  Pred. No. 5.5e-34;
  Matches  288;  Conservative    0;  Mismatches  211;  Indels    0;  Gaps    0;

Qy          3 CAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGGAT 62
Db         31 CAGAGAACACAGCGCAGCACGGAAATTCTACGAGACCTGACGGACAGGAACATCTCCGAC 90

Qy         63 TATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTG 122
Db         91 TTCTTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTC 150

Qy        123 AATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCG 182
Db        151 AATGAACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACG 210

Qy        183 AGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGAC 242
Db        211 GGGGAAGCACTTGTTGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGC 270

Qy        243 AGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGA 302
Db        271 CCTATCACTAGAGAGGCCTCTAAAGAAATACCTGATTTCCTTAAACATCTAGAAACTGAA 330

Qy        303 AATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAAT 362
Db        331 GACAACATTAAGGTGTGGTTTAATAACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAAT 390

Qy        363 GTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTAT 422
Db        391 GTGGCCCACAACGCCATCTTACGGGCCAGCCTGCCTAAGGACAGGAGCCCCGAGGAGTAT 450

Qy        423 GGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCT 482
Db        451 GGAATCACCGTCATTAGCCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATTACA 510
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Qy    483 CTGATGACCACATCAGTGG 501
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Db    511 GTGCTGACCACTTCAGTGG 529


RESULT 5
BE786243
LOCUS       BE786243               1132 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601474378F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877387 5',
            mRNA sequence.
ACCESSION   BE786243
VERSION     BE786243.1  GI:10207441
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1132)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9639  row: k  column: 20
            High quality sequence stop: 695.
FEATURES             Location/Qualifiers
     source          1. .1132
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3877387"
                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      324 a    275 c    311 g    222 t
ORIGIN

  Query Match           28.5%;  Score 142.8;  DB 12;  Length 1132;
  Best Local Similarity   55.4%;  Pred. No. 7.9e-29;
  Matches  276;  Conservative    0;  Mismatches  222;  Indels    0;  Gaps    0;

Qy      4 AAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGGATT 63
          | |||| |||   ||   | || || || || |||      |||    |   |
Db      7 AGAGAACACAGCGCAGCACGGAAATTCTACAAGACGCTGACGGACAGGAACATCTCCGAC 66

Qy     64 ATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGA 123
           |||||| || ||||||       | |||   |  |||||||||| |||  ||||||| |
Db     67 TTCTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCA 126

Qy    124 ATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGA 183
          ||||    |||||||| ||  ||||| | || |  |      |    |  |      ||
Db    127 ATGAACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGG 186

Qy    184 GTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACA 243
          |  ||| | ||   |      | |   |  |          | ||  ||  |  || |
Db    187 GGGAAGCACTTGTGGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCC 246

Qy    244 GTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAA 303
          |  |      ||    |      ||  | | |   || || ||   |
Db    247 CTATCACTAGAGAGGCCTCTAAAGAAATACCTGATTTCCTTAAACATCTAGAAACTGAAG 306

Qy    304 ATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATG 363
          | ||  | ||||||||||| |||||||| ||||||||||  |   |   || || ||||
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Db    307 ACAACATTAAGGTGTGGTTTAATAACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATG 366

Qy    364 TCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATG 423
          |   | |||| ||||| | ||||||| |||||  ||||    || |||     | ||||
Db    367 TGGCCCACAACGCCATCTTACGGGCCAGCCTGCCTAAGGACAGGAGCCCCGAGGAGTATG 426

Qy    424 GAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTC 483
          |||| || |   | |  || |||||||| || |||||| |||||||||||||| | |
Db    427 GAATCACCGTCATTAGCCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATTACAG 486

Qy    484 TGATGACCACATCAGTGG 501
          || ||||||| |||||||
Db    487 TGCTGACCACTTCAGTGG 504


RESULT 6
BQ948089
LOCUS       BQ948089                882 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8800681 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6392328
            5', mRNA sequence.
ACCESSION   BQ948089
VERSION     BQ948089.1  GI:22363567
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13882  row: a  column: 01
            High quality sequence stop: 768.
FEATURES             Location/Qualifiers
     source          1. .882
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6392328"
                     /clone_lib="NIH_MGC_130"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
                     Primer: Oligo dT.  Average insert size 1.95  kb.
                     Constructed by ResGen, Invitrogen Corp. Note: this is a
                     NIH_MGC Library."
BASE COUNT      176 a    269 c    251 g    185 t      1 others
ORIGIN

  Query Match           25.5%;  Score 127.6;  DB 14;  Length 882;
  Best Local Similarity   55.6%;  Pred. No. 1.2e-24;
  Matches  266;  Conservative    0;  Mismatches  209;  Indels    3;  Gaps    1;

Qy     24 GATATCCTTCAGGACCTGACAGGAAGAAACATTTCGGATTATCTGGTGAAGACGTATGTG 83
          ||  |  | ||| |||| || ||  ||||  | || || | | ||||||||||| ||
Db    332 GAGGTGGTCCAGAACCTCACTGGCCGAAATGTGTCTGACTTTTTGGTGAAGACATACCCC 391

Qy     84 CAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGC 143
             |  |  | || ||||| |||||  |||||| ||||| | || ||||| |||
Db    392 AGCCTGGTGCGCCGAGGCCTAAAGACCAAGAAGTGGGTGGATGAGGTCAGATATGGGGGC 451

Qy    144 TTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCC 203
          || |||||||| | | |  |  || ||  || ||  |  | || || ||        |
Db    452 TTCTCCCTGGGAGGCCGAGA---TCCAGACCTGCCCACAGGGCATGAGGTGGTCCGCACA 508
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```
Qy     204 ATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTC 263
Db     509 TTGGCAGAGATTCGGGCACTGCTGAGCCCCCAACCTGGGAATGCGCTAGACCGTATCCTG 568

Qy     264 AACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTC 323
Db     569 AACAACCTCACTCAGTGGGCCCTTGGCCTTGATGCTCGGAACAGCCTCAAGATCTGGTTC 628

Qy     324 AATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTC 383
Db     629 AACAACAAGGGCTGGCATGCCATGGTGGCCTTTGTGAACCGAGCCAACAATGGACTCCTA 688

Qy     384 CGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCAT 443
Db     689 CATGCCCTCCTACCATCTGGTCCAGTCCGCCATGCCCACAGCATCACTACACTCAACCAT 748

Qy     444 CCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 501
Db     749 CCTTTGAACTTGACCAAGGAGCAGCTATCTGAAGCTACACTGATAGCTCCCCCTCTGG 806
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RESULT 7
U66691
LOCUS U66691 2640 bp mRNA linear HTC 23-JUL-2001
DEFINITION Homo sapiens clone EST394388 mRNA sequence.
ACCESSION U66691
VERSION U66691.1 GI:1906576
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2640)
AUTHORS Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
TITLE Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PUBMED 8894702
REFERENCE 2 (bases 1 to 2640)
AUTHORS Allikmets,R., Gerrard,B. and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES Location/Qualifiers
source 1. .2640
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="EST394388"
/note="similar to ATP-binding cassette transporter"
BASE COUNT 607 a 672 c 667 g 647 t 47 others
ORIGIN

Query Match 23.7%; Score 118.8; DB 11; Length 2640;
Best Local Similarity 55.8%; Pred. No. 4.3e-22;
Matches 242; Conservative 0; Mismatches 191; Indels 1; Gaps 1;

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Qy      69 GTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAG 128
Db     988 GNGAGTANNNATCCTGCTCTTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCAATGAA 1047

Qy     129 TTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAA 188
Db    1048 CAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGGGGGAA 1107

Qy     189 GAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCT 248
Db    1108 GCACTTGTTGGGTTTTTAAGCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCCCTATC 1167

Qy     249 GCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAAT 308
Db    1168 ACTAGAGAGGCCTCTAAAGAAATACCTGATTTCCTTAAACATCTAGAAACTGAAGACAAC 1227
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Qy     309 GTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATC 368
Db    1228 ATTAAGGTGTGGTTTAATAACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATGTGGCC 1287

Qy     369 AACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATT 428
Db    1288 CACAACGCCATCTTACGGGCCAGCCTGCCTAAGGACAGGAGCCCCGAGGAGTATGGAATC 1347

Qy     429 ACTGCTTTCAATCATCCCCTGAATCT-CACCAAGCAGCAGCTCTCAGAGGTGGCTCTGAT 487
Db    1348 ACCGTCATTAGCCAACCCCTGAACCTGGACCAAGGAGCAGCTCTCAGAGATTACAGTGCT 1407

Qy     488 GACCACATCAGTGG 501
Db    1408 GACCACTTCAGTGG 1421
```

RESULT 8
BM687039
LOCUS BM687039 423 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CQ1-acx-g-10-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone UI-E-CQ1-acx-g-10-0-UI 5', mRNA sequence.
ACCESSION BM687039
VERSION BM687039.1 GI:19000297
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-acx-g-10-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAAGTG. This library was created for the program, Gene

Discovery in the Visual System, supported by National Eye Institute (NEI)."
BASE COUNT 107 a 111 c 106 g 99 t
ORIGIN

Query Match 22.2%; Score 111; DB 14; Length 423;
Best Local Similarity 68.6%; Pred. No. 4e-20;
Matches 153; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```
Qy    279 TTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGG 338
          ||  | | |   || || ||   | | ||  | |||||||||| |||||||| ||||||
Db     80 TTCCTTAAACATCTAGAAACTGAAGACAACATTAAGGTGTGGTTTAATAACAAAGGCTGG 139

Qy    339 CATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAA 398
          |||||  |   |   || || |||||   | |||| |||||  | |||||| |||||
Db    140 CATGCCCTGGTCAGCTTTCTCAATGTGGCCCACAACGCCATCTTACGGGCCAGCCTGCCT 199

Qy    399 AAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACC 458
          ||||    || |||     | |||||||| || |   | |  || |||||||| || |||
Db    200 AAGGACAGGAGCCCCGAGGAGTATGGAATCACCGTCATTAGCCAACCCCTGAACCTGACC 259

Qy    459 AAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||| |  |  || |||||| ||||||
Db    260 AAGGAGCAGCTCTCAGAGATTACAGTGCTGACCACTTCAGTGG 302
```

RESULT 9
W26316/c
LOCUS W26316 452 bp mRNA linear EST 08-MAY-1996
DEFINITION 27g5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence.
ACCESSION W26316
VERSION W26316.1 GI:1307006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 452)
AUTHORS Macke, J., Smallwood, P. and Nathans, J.
TITLE Adult Human Retina cDNA
JOURNAL Unpublished (1996)
COMMENT Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRimers
FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAATT.
FEATURES Location/Qualifiers
source 1. .452
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
/tissue_type="retina"
/dev_stage="adult"
/lab_host="E. coli strain K802"
/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI; Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library. Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, size-selected, and cloned into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."
BASE COUNT 111 a 100 c 123 g 113 t 5 others
ORIGIN

Query Match 22.0%; Score 110; DB 14; Length 452;
Best Local Similarity 68.2%; Pred. No. 7.7e-20;
Matches 152; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy    279 TTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGG 338
          ||  | | |   |  || ||   | | ||  | |||||||||| |||||||| ||||||
Db    405 TTCCTTAAACATCNAGAAACTGAAGACAACATTAAGGTGTGGTTTAATAACAAAGGCTGG 346

Qy    339 CATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAA 398
          |||||  |   |   || || |||||   | |||| |||||  | |||||| |||||
Db    345 CATGCCCTGGTCAGCTTTCTCAATGTGGCCCACAACGCCATCTTACGGGCCAGCCTGCCT 286

Qy    399 AAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACC 458
          ||||    || |||     | |||||||| || |   | |  || |||||||| || |||
Db    285 AAGGACAGGAGCCCCGAGGAGTATGGAATCACCGTCATTAGCCAACCCCTGAACCTGACC 226

Qy    459 AAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 501
          ||| ||||||||||||||| |  |  || |||||| ||||||
Db    225 AAGGAGCAGCTCTCAGAGATTACAGTGCTGACCACTTCAGTGG 183
```

RESULT 10
AW380897
LOCUS AW380897 412 bp mRNA linear EST 04-FEB-2000
DEFINITION CM3-HT0283-281099-028-h10 HT0283 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW380897
VERSION AW380897.1 GI:6885556
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0283-281099-028-h10&t3=1999-10-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 412.
FEATURES Location/Qualifiers
source 1. .412
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0283"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 92 a 118 c 84 g 118 t
ORIGIN

Query Match 19.9%; Score 99.8; DB 10; Length 412;
Best Local Similarity 98.1%; Pred. No. 5e-17;
Matches 101; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy    399 AAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACC 458
```

```
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     42 AAAAGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACC 101

Qy    459 AAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 501
          |||||||||||||||||||||||||||||||||||||||||||
Db    102 AAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 144


RESULT 11
BI063291/c
LOCUS       BI063291                281 bp    mRNA    linear   EST 15-JUN-2001
DEFINITION  IL3-UT0117-300301-538-A01 UT0117 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI063291
VERSION     BI063291.1  GI:14470818
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 281)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-UT0117-
            300301-538-A01&t3=2001-03-30&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 281.
FEATURES             Location/Qualifiers
     source          1. .281
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="UT0117"
                     /dev_stage="Adult"
                     /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       49 a     72 c     77 g     83 t
ORIGIN

  Query Match             19.6%;  Score 98.4;  DB 13;  Length 281;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-16;
  Matches   99;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 CACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCGG 41

Qy     61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAG 100
          ||||  ||||||||||||||||||||||||||||||||||
Db     40 ATTACCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAG 1


RESULT 12
AW322690
LOCUS       AW322690                434 bp    mRNA    linear   EST 26-JAN-2000
DEFINITION  uo51b11.y1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:2646045 5'
            similar to gb:X75926 M.musculus abc1 mRNA (MOUSE);, mRNA sequence.
ACCESSION   AW322690
VERSION     AW322690.1  GI:6756715
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Other_ESTs: uo51b11.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            MGI:1026497
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Mus musculus"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2646045"
                     /clone_lib="NCI_CGAP_Lu29"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT       83 a    127 c     95 g    129 t
ORIGIN

  Query Match             18.0%;  Score 90.2;  DB 10;  Length 434;
  Best Local Similarity   88.3%;  Pred. No. 2.3e-14;
  Matches   98;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    391 ACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGA 450
          ||||||| |||||||||||||| ||||| |||||||| |||||||||| || ||| |||
Db      1 ACCTGCAGAAGGGAGAGAACCCGAGCCAGTATGGAATCACTGCTTTCAACCACCCCTTGA 60

Qy    451 ATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGG 501
          | ||||| || ||||||||||||||||||||||||||||||| || || |
Db     61 ACCTCACTAAACAGCAGCTCTCAGAGGTGGCTCTGATGACCACCTCTGTCG 111


RESULT 13
CNS03550/c
LOCUS       CNS03550                857 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            213C18 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL228285
VERSION     AL228285.1  GI:7887267
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 857)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 857)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .857
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="213C18"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG213BB09LP1-end : T7"
BASE COUNT      209 a    221 c    260 g    165 t      2 others
ORIGIN

  Query Match             17.6%;  Score 88.2;  DB 17;  Length 857;
  Best Local Similarity   69.4%;  Pred. No. 9.8e-14;
  Matches  120;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy    313 AGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACA 372
          ||||||||| |||||||||||||||||| || ||     | ||| |||| ||    ||||
Db    574 AGGTGTGGTACAATAACAAGGGCTGGCACGCCATGGTGGCCTTCATGAACGTGGCTAACA 515

Qy    373 ATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTG 432
          | ||||| || || || |||||||     || |  ||||    | |  | || || || |
Db    514 ACGCCATCCTGCGCGCGAACCTGCCCCCAGGGGCCAACCTGGCCGAACACGGCATCACGG 455

Qy    433 CTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 485
             |||| ||||| ||||| || |||||| ||||||| || ||| |  || ||
Db    454 TGATCAACCATCCTCTGAACCTGACCAAGGAGCAGCTGTCCGAGATCACTGTG 402


RESULT 14
CNS02FFT
LOCUS       CNS02FFT                875 bp    DNA     linear   GSS 13-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            132012 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL194978
VERSION     AL194978.1  GI:7833084
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 875)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 875)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .875
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="132012"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG132BH06SP1-end :
                     PUC-Ori"
BASE COUNT      179 a    243 c    238 g    206 t      9 others
ORIGIN

  Query Match             17.5%;  Score 87.8;  DB 17;  Length 875;
  Best Local Similarity   68.8%;  Pred. No. 1.3e-13;
  Matches  119;  Conservative    1;  Mismatches   53;  Indels    0;  Gaps    0;

Qy    313 AGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACA 372
          ||||||||| |||||||||:||||||| || ||     | ||| |||| ||    ||||
Db    475 AGGTGTGGTACAATAACAASGGCTGGCACGCCATGGTGGCCTTCATGAACGTGGCTAACA 534

Qy    373 ATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTG 432
          | ||||| || || || |||||||     || |  ||||    | |  | || || || |
Db    535 ACGCCATCCTGCGCGCGAACCTGCCCCCAGGGGCCAACCTGGCCGAACACGGCATCACGG 594

Qy    433 CTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 485
             |||| ||||| ||||| || |||||| ||||||| || ||| |  || ||
Db    595 TGATCAACCATCCTCTGAACCTGACCAAGGAGCAGCTGTCCGAGATCACTGTG 647


RESULT 15
H87069
LOCUS       H87069                  426 bp    mRNA    linear   EST 21-NOV-1995
DEFINITION  ys74d05.r1 Soares retina N2b4HR Homo sapiens cDNA clone
            IMAGE:220521 5', mRNA sequence.
ACCESSION   H87069
VERSION     H87069.1  GI:1068648
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 330
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
           Insert Length: 1209   Std Error: 0.00
           Seq primer: M13RP1
           High quality sequence stop: 330.
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="GDB:3848514"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:220521"
                     /clone_lib="Soares retina N2b4HR"
                     /sex="male"
                     /tissue_type="retina"
                     /dev_stage="55 year old"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). The retinas were obtained from a 55 year old
                     Caucasian  and total cellular poly(A)+ RNA was extracted 6
                     hrs after their removal. The retina RNA  was kindly
                     provided by Roderick R. McInnes M.D. Ph.D. from the
                     University  of Toronto. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. "
BASE COUNT      117 a    100 c    105 g    101 t      3 others
ORIGIN

  Query Match             16.7%;  Score 83.8;  DB 14;  Length 426;
  Best Local Similarity   54.1%;  Pred. No. 1.4e-12;
  Matches  213;  Conservative    0;  Mismatches  178;  Indels    3;  Gaps    2;

Qy      88 TCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTT 147
           | |||   |  |||||||||| |||  ||||||| |||||    |||||||| ||  |||
Db      11 TTATAAGAAGCAGCTTAAAGAGCAAATTCTGGGTCAATGAACAGAGGTATGGAGGAATTT 70

Qy     148 CCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCA 207
           || | || |  |      |    |  |      || |  ||| | ||  ||      | ||
Db      71 CCATTGGAGGAAAGCTCCCAGTCGTCCCCATCACGGGGGAAGCACTTGTTGGGTTTTTAA 130

Qy     208 AACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACA 267
              |  |         | | ||  ||  |  || |  |    |             ||
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Qy     268 GCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATA 327
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Qy     328 ACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGG 387
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GenCore version 5.1.4_p5_4578

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Run on: April 3, 2003, 09:40:44 ; Search time 992.885 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		501	100.0	2617	6	AX059974	AX059974 Sequence
2		501	100.0	2894	6	AX127797	AX127797 Sequence
3		501	100.0	2894	6	AX139784	AX139784 Sequence
4		501	100.0	3366	6	AX060718	AX060718 Sequence
5		501	100.0	3366	6	AX060897	AX060897 Sequence
6		501	100.0	5352	6	AX127778	AX127778 Sequence
7		501	100.0	5352	6	AX139765	AX139765 Sequence
8		501	100.0	9495	6	AX059978	AX059978 Sequence
9		501	100.0	9497	6	AX059973	AX059973 Sequence
10		501	100.0	9497	9	AF165281	AF165281 Homo sapi
11		501	100.0	9593	6	AX059976	AX059976 Sequence
12		501	100.0	9741	6	AX127830	AX127830 Sequence
13		501	100.0	9741	6	AX139817	AX139817 Sequence
14		501	100.0	9741	6	AX351038	AX351038 Sequence
15		501	100.0	9854	6	AX127831	AX127831 Sequence
16		501	100.0	9854	6	AX139818	AX139818 Sequence
17		501	100.0	10442	6	AX060713	AX060713 Sequence
18		501	100.0	10442	6	AX060892	AX060892 Sequence
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21		501	100.0	10474	6	AX060721	AX060721 Sequence
22		501	100.0	10474	6	AX060898	AX060898 Sequence
23		501	100.0	10474	6	AX060900	AX060900 Sequence
24		490	97.8	7860	6	AX092594	AX092594 Sequence
25		490	97.8	7862	6	AX135712	AX135712 Sequence
26	c	490	97.8	129608	9	AL353685	AL353685 Human DNA
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37		197.4	39.4	7878	10	MMABC1	X75926 Mus musculu
38		197.4	39.4	186889	2	AL807243	AL807243 Mus muscu
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40		197.4	39.4	230272	2	AL772397	AL772397 Mus muscu
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ALIGNMENTS

RESULT 1
AX059974
LOCUS AX059974 2617 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 92 from Patent WO0078970.
ACCESSION AX059974
VERSION AX059974.1 GI:12405632
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2617)
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.

```
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 92 28-DEC-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .2617
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      840 a    459 c    435 g    883 t
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  Best Local Similarity   100.0%;  Pred. No. 3.4e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
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Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Qy     481 CTGGTGGCAGTAACATGCAAC 501
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RESULT 2
AX127797
LOCUS       AX127797                2894 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 36 from Patent WO0130848.
ACCESSION   AX127797
VERSION     AX127797.1  GI:14134444
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2894)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 36 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .2894
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.4e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
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Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
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Qy     481 CTGGTGGCAGTAACATGCAAC 501
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Db     795 CTGGTGGCAGTAACATGCAAC 815


RESULT 3
AX139784
LOCUS       AX139784                2894 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 36 from Patent EP1096012.
ACCESSION   AX139784
VERSION     AX139784.1  GI:14275366
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2894)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleics acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: EP 1096012-A 36 02-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .2894
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  Query Match             100.0%;  Score 501;  DB 6;  Length 2894;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-115;
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Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db    795 CTGGTGGCAGTAACATGCAAC 815


RESULT 4
AX060718
LOCUS       AX060718               3366 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 6 from Patent WO0078972.
ACCESSION   AX060718
VERSION     AX060718.1  GI:12406107
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3366)
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 6 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .3366
                     /organism="Homo sapiens"
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  Best Local Similarity   100.0%;  Pred. No. 3.3e-115;
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RESULT 5
AX060897
LOCUS       AX060897               3366 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 6 from Patent WO0078971.
ACCESSION   AX060897
VERSION     AX060897.1  GI:12406274
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3366)
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 6 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
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BASE COUNT     1119 a    564 c    559 g   1120 t      4 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 3366;
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Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db    174 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 233

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 293

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 353

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 413
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Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 473

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 533

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 593

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 653

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    654 CTGGTGGCAGTAACATGCAAC 674
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RESULT 6
AX127778
LOCUS       AX127778               5352 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 17 from Patent WO0130848.
ACCESSION   AX127778
VERSION     AX127778.1  GI:14134425
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5352)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 17 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .5352
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1675 a    928 c    976 g   1772 t      1 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 5352;
  Best Local Similarity  100.0%;  Pred. No. 3e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 568

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 628

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 688

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
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Db    689 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 748

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 808

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 868

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 928

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db    929 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 988

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    989 CTGGTGGCAGTAACATGCAAC 1009
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RESULT 7
AX139765
LOCUS       AX139765               5352 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 17 from Patent EP1096012.
ACCESSION   AX139765
VERSION     AX139765.1  GI:14275347
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5352)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleics acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: EP 1096012-A 17 02-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .5352
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1675 a    928 c    976 g   1772 t      1 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 5352;
  Best Local Similarity  100.0%;  Pred. No. 3e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db    509 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 568

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 628

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 688

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 748

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 808

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 868

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 928
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Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db    929 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 988

Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db    989 CTGGTGGCAGTAACATGCAAC 1009
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RESULT 8
AX059978
LOCUS       AX059978               9495 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 96 from Patent WO0078970.
ACCESSION   AX059978
VERSION     AX059978.1  GI:12405636
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9495)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 96 28-DEC-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9495
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2599 a   2115 c   2216 g   2564 t      1 others
ORIGIN

  Query Match            100.0%;  Score 501;  DB 6;  Length 9495;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6898 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 6957

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6958 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7017

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Db   7018 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7077

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7078 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7137

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7138 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7197

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7198 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7257

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7258 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7317

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db   7318 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7377

Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db   7378 CTGGTGGCAGTAACATGCAAC 7398
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RESULT 9
AX059973
LOCUS       AX059973               9497 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 91 from Patent WO0078970.
ACCESSION   AX059973
VERSION     AX059973.1  GI:12405631
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 91 28-DEC-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9497
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2600 a   2115 c   2217 g   2564 t      1 others
ORIGIN

  Query Match            100.0%;  Score 501;  DB 6;  Length 9497;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6900 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 6959

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6960 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7019

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7020 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7079

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7080 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7139

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7140 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7199

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7200 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7259

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
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Db   7260 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7319

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db   7320 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7379

Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db   7380 CTGGTGGCAGTAACATGCAAC 7400
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RESULT 10
AF165281
LOCUS       AF165281               9497 bp    mRNA    linear   PRI 17-AUG-1999
DEFINITION  Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA,
            complete cds.
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ACCESSION   AF165281
VERSION     AF165281.1  GI:5734100
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Tangier disease is caused by mutations in the gene encoding
            ATP-binding cassette transporter 1
  JOURNAL   Nat. Genet. 22 (4), 352-355 (1999)
  MEDLINE   99364413
   PUBMED   10431238
REFERENCE   2  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
            Cr#mieux, Evry 91006, France
FEATURES             Location/Qualifiers
     source          1. .9497
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9q31"
     gene            1. .9497
                     /gene="ABC1"
     CDS             121. .6726
                     /gene="ABC1"
                     /note="ABC transporter; ABC1 protein"
                     /codon_start=1
                     /product="ATP cassette binding transporter 1"
                     /protein_id="AAD49849.1"
                     /db_xref="GI:5734101"
                     /translation="MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVAR
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                     KLAAAERVLRSNMDILKPILRTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSW
                     SDMRQEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGG
                     NGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQ
                     VMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQ
                     LDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLNKL
                     EPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERTNK
                     IKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQQMPYPC
                     YVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILWFS
                     WFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLFSR
                     ANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCEYFALFEEQ
                     GIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYIEAVFPGQYGIPRPWYF
                     PCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVSIQNLVKVYRDGMKVAV
                     DGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQN
                     LGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKTSQ
                     LSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQGRTIILSTHH
                     MDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLSSCRNSSST
                     VSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHELTY
                     VLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETSDG
                     TLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVKGW
                     KLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ
                     PWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEWTT
                     APVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADI
                     LQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDA
                     TKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNA
                     ILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPA
                     SFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKS
                     YVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF
                     VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPL
                     SWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRI
                     LDGGGQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLT
                     GDTTVTRGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPE
                     KEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMD
                     PKARRFLWNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNR
                     FGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVPKEKHRNMLQYQLPSSLSSLARIFS
                     ILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSF
                     LQDEKVKESYV"
BASE COUNT      2600 a    2115 c    2217 g    2564 t       1 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 9;  Length 9497;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6900 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 6959

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6960 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7019

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7020 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7079

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7080 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7139

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7140 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7199

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7200 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7259

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7260 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7319

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7320 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7379

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    7380 CTGGTGGCAGTAACATGCAAC 7400


RESULT 11
AX059976
LOCUS       AX059976                9593 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 94 from Patent WO0078970.
ACCESSION   AX059976
VERSION     AX059976.1  GI:12405634
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9593)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
            and Brewer,H.B.
  TITLE     Nucleic and proteinic acids corresponding to human gene abc1
  JOURNAL   Patent: WO 0078970-A 94 28-DEC-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9593
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      2616 a    2154 c    2237 g    2585 t       1 others
ORIGIN

  Query Match             100.0%;  Score 501;  DB 6;  Length 9593;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
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  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6996 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7055

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7056 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7115

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7116 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7175

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7176 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7235

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7236 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7295

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7296 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7355

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7356 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7415

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7416 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7475

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7476 CTGGTGGCAGTAACATGCAAC 7496


RESULT 12
AX127830
LOCUS       AX127830               9741 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 69 from Patent WO0130848.
ACCESSION   AX127830
VERSION     AX127830.1  GI:14134477
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9741)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 69 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2650 a   2180 c   2290 g   2620 t      1 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 9741;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 13
AX139817
LOCUS       AX139817               9741 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 69 from Patent EP1096012.
ACCESSION   AX139817
VERSION     AX139817.1  GI:14275399
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9741)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., searfoss Iii,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleics acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: EP 1096012-A 69 02-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2650 a   2180 c   2290 g   2620 t      1 others
ORIGIN

  Query Match           100.0%;  Score 501;  DB 6;  Length 9741;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 14
AX351038
LOCUS       AX351038               9741 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 10 from Patent WO0183746.
ACCESSION   AX351038
VERSION     AX351038.1  GI:18616393
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denefle,P.,
            Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
  TITLE     Regulatory nucleic acid sequences of the abc1 gene
  JOURNAL   Patent: WO 0183746-A 10 08-NOV-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2650 a    2180 c    2290 g    2620 t      1 others
ORIGIN

  Query Match            100.0%;  Score 501;  DB 6;  Length 9741;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 15
AX127831
LOCUS       AX127831               9854 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 70 from Patent WO0130848.
ACCESSION   AX127831
VERSION     AX127831.1  GI:14134478
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9854)
  AUTHORS   Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
            Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
            Remaley,A., Brewer,H.B. and Dean,M.
  TITLE     Nucleic acids of the human abc1 gene and their therapeutic and
            diagnostic application
  JOURNAL   Patent: WO 0130848-A 70 03-MAY-2001;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .9854
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2665 a    2219 c    2334 g    2635 t      1 others
ORIGIN

  Query Match            100.0%;  Score 501;  DB 6;  Length 9854;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-115;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7257 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7316

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7317 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7376

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7377 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7436

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7437 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7496

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7497 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7556

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7557 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7616
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Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7617 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7676

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7677 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7736

Qy     481 CTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7737 CTGGTGGCAGTAACATGCAAC 7757
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GenCore version 5.1.4_p5_4578

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Perfect score: 501
Sequence: 1 ttacaggggcagtgcctttg.....tggtggcagtaacatgcaac 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	501	100.0	3366	22	AAF24684	Nucleotide sequenc
	2	501	100.0	3366	22	AAF24706	Nucleotide sequenc
	3	501	100.0	5352	22	AAS04049	Human ABC1 gene, p
	4	501	100.0	9741	22	AAS06120	Human ABC1 DNA seq
	5	501	100.0	9741	24	AAD37273	Human ABC1 full-le
	6	501	100.0	9854	22	AAS06121	Human ABC1 DNA seq
	7	501	100.0	10442	22	AAF24680	Nucleotide sequenc
	8	501	100.0	10442	22	AAF24702	Nucleotide sequenc
	9	501	100.0	10474	22	AAF24685	Nucleotide sequenc
	10	501	100.0	10474	22	AAF24686	Nucleotide sequenc
	11	501	100.0	10474	22	AAF24707	Nucleotide sequenc
	12	501	100.0	10474	22	AAF24708	Nucleotide sequenc
	13	490	97.8	5138	21	AAC69147	Human ABC1 gene ex
	14	490	97.8	7857	21	AAC69388	Human ABC1 cholest
	15	490	97.8	7860	22	AAF83826	Human ABC1 nucleot
	16	490	97.8	7860	22	AAF92835	Human ABC1 cDNA.
	17	490	97.8	7861	21	AAC69387	Human ABC1 cholest
	18	490	97.8	7864	21	AAC69120	Human ABC1 cholest
	19	490	97.8	7864	21	AAC69385	Human ABC1 cholest
	20	490	97.8	7864	21	AAC69386	Human ABC1 cholest
	21	490	97.8	7864	21	AAC69389	Human ABC1 cholest
	22	490	97.8	183999	22	AAF92831	Human ABC1 genomic
	23	479.4	95.7	5097	22	AAI93913	Human stomach canc
	24	479.4	95.7	5097	22	AAH18233	Human cDNA sequenc
	25	479.2	95.6	2011	22	AAF24683	Nucleotide sequenc
	26	479.2	95.6	2011	22	AAF24705	Nucleotide sequenc
	27	178	35.5	748	22	AAF24682	Nucleotide sequenc
	28	178	35.5	748	22	AAF24704	Nucleotide sequenc
	29	48.6	9.7	65	24	ABN53927	Mouse spliced tran
	30	42.2	8.4	18512	24	ABL32976	Human immune syste
	31	39.4	7.9	518	24	ABQ15316	Oligonucleotide fo
c	32	39.4	7.9	518	24	ABQ15317	Oligonucleotide fo
	33	39	7.8	14307	24	ABL32728	Human immune syste
	34	38.8	7.7	16602	24	ABN80068	Human chemically m
	35	38.8	7.7	16602	24	ABL32726	Human immune syste
	36	38.8	7.7	18357	24	ABQ67083	Human angiogenesis
c	37	38.4	7.7	6197	23	ABL04066	Drosophila melanog
c	38	37.8	7.5	1380	24	ABA91277	Cryptosporidium pa
c	39	37.8	7.5	30610	22	ABA15643	Human nervous syst
c	40	37.6	7.5	600	20	AAV86185	EST clone J635. H
	41	37.6	7.5	804	22	AAI94638	Human neuroblastom
	42	37.4	7.5	5689	22	AAS45384	Chemically pretrea
	43	37.4	7.5	5689	22	AAS46426	Tumour suppressor
	44	37.4	7.5	5689	24	ABK28226	DNA transcription
	45	37.4	7.5	10468	23	ABL05156	Drosophila melanog

ALIGNMENTS

RESULT 1
AAF24684
ID AAF24684 standard; DNA; 3366 BP.
XX
AC AAF24684;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of the 3' flanking region of the human ABC1 gene.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI; 2001-137812/14.

```
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 146-148; 215pp; English.
XX
CC   The present sequence represents the 3' flanking region of the huuman
CC   adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
CC   resides in cell membranes and utilises ATP hydrolysis to transport a wide
CC   variety of substrates across the plasma membrane. ABC1 is a pivotal
CC   protein in the apolipoprotein-mediated mobilisation of intracellular
CC   cholesterol stores. ABC1 is defective in Tangier disease, a genetic
CC   disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
CC   gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
CC   are useful for developing pharmaceutical agents for the treatment of
CC   heart disease and other disorders associated with hypercholesterolemia
CC   and atherosclerosis. The genes are useful for developing screening assays
CC   to screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 3366;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-130;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     174 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 233

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 293

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 353

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 413

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 473

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
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Db     474 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 533

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 593

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db     594 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 653

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db     654 CTGGTGGCAGTAACATGCAAC 674


RESULT 2
AAF24706
ID   AAF24706 standard; DNA; 3366 BP.
XX
AC   AAF24706;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of the 3' flanking region of the human ABC1 gene.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 142-144; 211pp; English.
XX
CC   The present sequence represents the 3' flanking region of the huuman
CC   adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
CC   resides in cell membranes and utilises ATP hydrolysis to transport a wide
CC   variety of substrates across the plasma membrane. ABC1 is a pivotal
CC   protein in the apolipoprotein-mediated mobilisation of intracellular
CC   cholesterol stores. ABC1 is defective in Tangier disease, a genetic
CC   disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
CC   gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
CC   are useful for developing pharmaceutical agents for the treatment of
CC   heart disease and other disorders associated with hypercholesterolemia
CC   and atherosclerosis. The genes are useful for developing screening assays
CC   to screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 3366;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-130;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db     234 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 293

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 353

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 413
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Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 473

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
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Db    474 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 533

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
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Db    534 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 593

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db    594 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 653

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    654 CTGGTGGCAGTAACATGCAAC 674
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```
RESULT 3
AAS04049
ID   AAS04049 standard; DNA; 5352 BP.
XX
AC   AAS04049;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human ABC1 gene, partial genomic clone #15.
XX
KW   Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW   cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW   lecithin-cholesterol acetyltransferase; malaria; diabetes; ds.
XX
OS   Homo sapiens.
XX
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FT                   /partial
FT                   /note= "3' end of intron 48; this sequence is
FT                    specifically claimed"
FT                   /number= 48
FT   exon            195..3088
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FT                   /number= 49
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FT                   /note= "3' distal sequence"
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PN   WO200130848-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-EP10886.
XX
PR   26-OCT-1999;   99EP-0402668.
PR   01-MAR-2000; 2000US-0186260.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Denefle P,  Rosier-Montus M,  Arnould-Reguigne I,  Prades C,  Naudin L;
PI   Lemoine C,  Duverger N,  Jaye M,  Searfoss GH,  Remaley A,  Brewer HB;
PI   Dean M;
XX
DR   WPI; 2001-316327/33.
XX
PT   New human ABC1 nucleic acids and polypeptides for treating
PT   atherosclerosis, malaria and diabetes -
XX
PS   Claim 1; Page 179-182; 368pp; English.
XX
CC   The sequence represents the nucleic acid sequence of human ABC1 gene,
CC   partial genomic clone #15, comprising part of intron 48, exon 49,
CC   and 3' distal sequence. The nucleic acid sequence, primers and probes
CC   derived from the sequence, and polypeptides and vectors are useful for
CC   the prevention of atherosclerosis, in a subject affected by a dysfunction
CC   in the reverse transport of cholesterol. The polypeptide encoded by the
CC   ABC1 gene is useful for screening for an active ingredient for the
CC   prevention or treatment of a disease resulting from dysfunction in the
CC   reverse transport of cholesterol. The nucleic acids and polypeptides are
CC   also useful for treating and preventing cardiovascular and neurological
CC   pathologies, and other diseases e.g. Tangier disease, lecithin-
CC   cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ   Sequence 5352 BP; 1675 A; 928 C; 976 G; 1772 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 5352;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-130;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db    509 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 568

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db    569 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 628

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Db    629 TTGAACTCACACTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 688

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
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Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 928

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 988

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    989 CTGGTGGCAGTAACATGCAAC 1009
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RESULT 4
AAS06120
ID   AAS06120 standard; cDNA; 9741 BP.
XX
AC   AAS06120;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human ABC1 DNA sequence #1.
XX
KW   Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW   cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW   lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS   Homo sapiens.
XX
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FH   Key             Location/Qualifiers
FT   CDS             185..6967
FT                   /*tag= a
FT                   /product= "Human ABC1 protein"
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PN   WO200130848-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-EP10886.
XX
PR   26-OCT-1999;   99EP-0402668.
PR   01-MAR-2000; 2000US-0186260.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Denefle P,  Rosier-Montus M,  Arnould-Reguigne I,  Prades C,  Naudin L;
PI   Lemoine C,  Duverger N,  Jaye M,  Searfoss GH,  Remaley A,  Brewer HB;
PI   Dean M;
XX
DR   WPI; 2001-316327/33.
DR   P-PSDB; AAU02176.
XX
PT   New human ABC1 nucleic acids and polypeptides for treating
PT   atherosclerosis, malaria and diabetes -
XX
PS   Claim 1; Page 204-208; 368pp; English.
XX
CC   The sequence represents the coding sequence #1 of human ABC1. The
CC   nucleic acid sequence, primers and probes derived from the ABC1 sequence,
CC   and polypeptides and vectors are useful for the prevention of
CC   atherosclerosis, in a subject affected by a dysfunction in the reverse
CC   transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC   useful for screening for an active ingredient for the prevention or
CC   treatment of a disease resulting from dysfunction in the reverse
CC   transport of cholesterol. The nucleic acids and polypeptides are also
CC   useful for treating and preventing cardiovascular and neurological
CC   pathologies, and other diseases e.g. Tangier disease, lecithin-
CC   cholesterol (LCAT) deficiency, malaria and diabetes.
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SQ   Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 9741;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 5
AAD37273
ID   AAD37273 standard; cDNA; 9741 BP.
XX
AC   AAD37273;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human ABC1 full-length cDNA.
XX
KW   Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;
KW   cholesterol metabolism; hypercholesterolaemia; antisense therapy;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             185..6970
FT                   /*tag= a
FT                   /product= "Human ABC1 full-length protein"
XX
PN   WO200183746-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-EP05488.
XX
PR   02-MAY-2000; 2000US-201280P.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Rosier-Montus M,  Prades C,  Lemoine C,  Naudin L,  Denefle P;
PI   Brewer B,  Duverger N,  Remaley A,  Santamarina-Fojo S;
XX
DR   WPI; 2002-154404/20.
DR   P-PSDB; AAE23000.
XX
PT   Isolated nucleic acid useful for modifying the ATP-binding cassette 1
PT   (ABC1) and screening for candidate modulatory compounds or substances
PT   -
XX
PS   Example 1; Page 133-136; 152pp; English.
XX
CC   The invention relates a nucleic acid which is capable of regulating the
CC   transcription of human ATP-binding cassette 1 (ABC1) gene, which is a
CC   casual gene for pathologies linked to a dysfunctioning of cholesterol
CC   metabolism, including diseases such as atherosclerosis. Polynucleotides
CC   of the invention are used to screen candidate molecules or substances
CC   that are capable of modulating the transcription of the ABC1 gene. They
CC   are used in antisense therapy. Compositions comprising sequences of the
CC   invention are used to treat hypercholesterolaemia and atherosclerosis.
CC   The present sequence is human ABC1 full-length cDNA.
XX
SQ   Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

  Query Match             100.0%;  Score 501;  DB 24;  Length 9741;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203
```

```
Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy     481 CTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7624 CTGGTGGCAGTAACATGCAAC 7644
```

RESULT 6
AAS06121
ID AAS06121 standard; cDNA; 9854 BP.
XX
AC AAS06121;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human ABC1 DNA sequence #2.
XX
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 298..7078
FT /*tag= a
FT /product= "Human ABC1 protein"
XX
PN WO200130848-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-EP10886.
XX
PR 26-OCT-1999; 99EP-0402668.
PR 01-MAR-2000; 2000US-0186260.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI Dean M;
XX
DR WPI; 2001-316327/33.
DR P-PSDB; AAU02176.
XX
PT New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX
PS Claim 1; Page 209-213; 368pp; English.
XX
CC The sequence represents the coding sequence #2 of human ABC1. The
CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
CC and polypeptides and vectors are useful for the prevention of
CC atherosclerosis, in a subject affected by a dysfunction in the reverse
CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC useful for screening for an active ingredient for the prevention or
CC treatment of a disease resulting from dysfunction in the reverse
CC transport of cholesterol. The nucleic acids and polypeptides are also
CC useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
CC cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;

Query Match 100.0%; Score 501; DB 22; Length 9854;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7257 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7316

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7317 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7376

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7377 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7436

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7437 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7496

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7497 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7556

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7557 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7616

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7617 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7676

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7677 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7736

Qy     481 CTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7737 CTGGTGGCAGTAACATGCAAC 7757
```

RESULT 7
AAF24680
ID AAF24680 standard; DNA; 10442 BP.
XX
AC AAF24680;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI; 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 122-128; 215pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7250 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7309

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7310 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7369

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7370 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7429

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7430 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7489

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7490 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7549

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7550 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7609

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7610 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7669

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7670 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7729

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    7730 CTGGTGGCAGTAACATGCAAC 7750
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RESULT 8
AAF24702
ID AAF24702 standard; DNA; 10442 BP.
XX
AC AAF24702;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human ABC1 polypeptide.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
DR P-PSDB; AAB31365.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Claim 3; Page 117-123; 211pp; English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart

```
CC   disease and other disorders associated with hypercholesterolemia and
CC   atherosclerosis. The genes are useful for developing screening assays to
CC   screen for compounds that regulate the expression of genes associated
CC   with cholesterol transport. The genes and proteins are also useful for
CC   are also useful as diagnostic indicators of cardiovascular disease and
CC   other disorders associated with hypercholesterolemia.
XX
SQ   Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10442;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7250 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7309

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7310 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7369

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7370 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7429

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7430 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7489

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7490 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7549

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7550 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7609

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7610 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7669

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7670 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7729

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    7730 CTGGTGGCAGTAACATGCAAC 7750


RESULT 9
AAF24685
ID   AAF24685 standard; DNA; 10474 BP.
XX
AC   AAF24685;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 148-154; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

  Query Match             100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7282 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7341

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7342 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7401

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7402 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7461

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7462 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7521

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7522 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7581

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7582 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7641

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7642 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7701
```

```
Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7702 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7761

Qy     481 CTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7762 CTGGTGGCAGTAACATGCAAC 7782
```

```
RESULT 10
AAF24686
ID   AAF24686 standard; DNA; 10474 BP.
XX
AC   AAF24686;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078972-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16765.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
XX
PI   Lawn RM,  Wade D,  Garvin M;
XX
DR   WPI; 2001-137812/14.
XX
PT   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT   useful for the development of agents for the treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Disclosure; Page 170-176; 215pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
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  Query Match           100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7282 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7341

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7342 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7401

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7402 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7461

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7462 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7521

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7522 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7581

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7582 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7641

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7642 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7701

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7702 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7761

Qy     481 CTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7762 CTGGTGGCAGTAACATGCAAC 7782
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RESULT 11
AAF24707
ID   AAF24707 standard; DNA; 10474 BP.
XX
AC   AAF24707;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
```

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PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31366.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 27; Page 144-150; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

  Query Match          100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7282 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7341

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7342 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7401

Qy     121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7402 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7461

Qy     181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7462 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7521

Qy     241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7522 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7581

Qy     301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7582 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7641

Qy     361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7642 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7701

Qy     421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7702 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7761

Qy     481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    7762 CTGGTGGCAGTAACATGCAAC 7782
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RESULT 12
AAF24708
ID   AAF24708 standard; DNA; 10474 BP.
XX
AC   AAF24708;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW   Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW   apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW   chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW   atherosclerosis; cholesterol transport; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             323..7108
FT                   /*tag=  a
FT                   /product= "defective ABC1 polypeptide"
XX
PN   WO200078971-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US16591.
XX
PR   18-JUN-1999;   99US-0140264.
PR   14-SEP-1999;   99US-0153872.
PR   19-NOV-1999;   99US-0166573.
XX
PA   (CVTH-) CV THERAPEUTICS INC.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lawn RM,  Wade D,  Oram JF,  Garvin M;
XX
DR   WPI; 2001-137811/14.
DR   P-PSDB; AAB31367.
XX
PT   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT   polynucleotides and polypeptides, useful for treatment of heart disease
PT   and other disorders associated with hypercholesterolemia and
PT   atherosclerosis -
XX
PS   Claim 30; Page 165-172; 211pp; English.
XX
CC   The present sequence encodes a human adenosine triphosphate (ATP)
CC   binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC   a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC   ATP hydrolysis to transport a wide variety of substrates across the
CC   plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC   mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC   Tangier disease, a genetic disorder characterised by abnormal
CC   HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC   9q22-9q31. The ABC1 genes and proteins are useful for developing
CC   pharmaceutical agents for the treatment of heart disease and other
CC   disorders associated with hypercholesterolemia and atherosclerosis. The
CC   genes are useful for developing screening assays to screen for compounds
CC   that regulate the expression of genes associated with cholesterol
CC   transport. The genes and proteins are also useful for are also useful
CC   as diagnostic indicators of cardiovascular disease and other disorders
CC   associated with hypercholesterolemia.
XX
SQ   Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

  Query Match          100.0%;  Score 501;  DB 22;  Length 10474;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-129;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db   7282 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7341

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7342 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7401

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7402 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7461

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7462 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7521

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7522 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7581

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7582 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7641

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7642 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7701

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7702 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7761

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7762 CTGGTGGCAGTAACATGCAAC 7782
```

```
RESULT 13
AAC69147
ID   AAC69147 standard; DNA; 5138 BP.
XX
AC   AAC69147;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 gene exons 46-49.
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;   99US-0124702.
PR   08-JUN-1999;   99US-0138048.
PR   17-JUN-1999;   99US-0139600.
PR   01-SEP-1999;   99US-0151977.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON BIORESEARCH INC.
XX
PI   Hayden MR,  Wilson AR,  Pimstone SN;
XX
DR   WPI; 2000-587528/55.
XX
PT   New ABC1 polypeptide is useful for treating diseases associated with
PT   ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT   disease and cancer -
XX
PS   Disclosure; Fig 12; 229pp; English.
XX
CC   The invention relates to the human ABC1 cholesterol transporter protein
CC   (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC   a member of the ATP-binding cassette (ABC transporter) superfamily of
CC   proteins, and plays a crucial role in cholesterol transport, particularly
CC   intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC   involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC   located on chromosome 9q31, and mutations in this gene are associated
CC   with two genetic HDL (high density lipoprotein) deficiency disorders,
CC   Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC   are distinguishable in that TD is an autosomal recessive disorder, while
CC   FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC   cholesterol") in the blood correlate with a high risk of cardiovascular
CC   disease, particularly coronary artery disease, but also cerebrovascular
CC   disease, coronary restenosis, and peripheral vascular disease.
CC   Conversely, a high level of HDL has protective effects against
CC   cardiovascular disease. The invention provides genetic constructs and
CC   transgenic cells and non-human animals comprising human ABC1 nucleic
CC   acids, and methods of gene therapy for the treatment or prevention of
CC   cardiovascular disease comprising the administration of an expression
CC   vector encoding ABC1 or an active fragment thereof. The invention also
CC   encompasses compounds which mimic ABC1 activity, compounds which
CC   stimulate ABC1 expression and methods of screening for such compounds.
CC   It further relates to methods for determining whether a patient has an
CC   increased risk for cardiovascular disease due to polymorphisms in the
CC   ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC   or prevent cardiovascular disease, especially coronary artery disease,
CC   cerebrovascular disease, coronary restenosis or peripheral vascular
CC   disease. They may also be used in the treatment of diseases associated
CC   with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC   disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC   The invention specifically excludes proteins with the exact amino acid
CC   sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC   acid with the exact sequence as GenBank Accession No: AJ012376.1.
CC   The present sequence represents a fragment of the human ABC1 gene
CC   comprising exonic sequences.
XX
SQ   Sequence 5138 BP; 1537 A; 952 C; 1010 G; 1606 T; 33 other;
```

```
  Query Match             97.8%;  Score 490;  DB 21;  Length 5138;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-126;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3261 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 3320

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3321 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 3380

Qy     121 TTGAACTCACAC-TTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 179
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    3381 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 3440

Qy     180 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3441 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 3500

Qy     240 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3501 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 3560

Qy     300 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3561 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 3620
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Qy     360 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3621 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 3680

Qy     420 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3681 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 3740

Qy     480 TCTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    3741 TCTGGTGGCAGTAACATGCAAC 3762
```

RESULT 14
AAC69388
ID AAC69388 standard; cDNA; 7857 BP.
XX
AC AAC69388;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX
DR WPI; 2000-587528/55.
DR P-PSDB; AAB38107.
XX
PT New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT disease and cancer -
XX
PS Examples; Page -; 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC transporter associated with an altered cholesterol level and therefore an
CC altered risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 cDNA shown on pages 157-160.
XX
SQ Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;

Query Match 97.8%; Score 490; DB 21; Length 7857;
Best Local Similarity 99.8%; Pred. No. 1.3e-126;
Matches 501; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db    7031 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7090

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db    7091 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7150

Qy     121 TTGAACTCACAC-TTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 179
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    7151 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 7210

Qy     180 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7211 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 7270

Qy     240 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7271 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 7330

Qy     300 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7331 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 7390

Qy     360 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7391 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 7450

Qy     420 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7451 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 7510

Qy     480 TCTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7511 TCTGGTGGCAGTAACATGCAAC 7532
```

RESULT 15
AAF83826
ID AAF83826 standard; DNA; 7860 BP.
XX

```
AC   AAF83826;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human ABC1 nucleotide sequence.
XX
KW   ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
KW   LDL; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..3341
FT                   /*tag= a
FT                   /product= "partial ABC1 protein"
FT                   /note= "the coding sequence continues beyond nucleotide
FT                          3341, possibly till position 6860 as identified
FT                          by translating the present sequence; part of the
FT                          corresponding protein is missing and nucleotide
FT                          3341 corresponds to the last amino acid residue
FT                          (position 1089) as indicated in the
FT                           specification"
XX
PN   WO200132184-A2.
XX
PD   10-MAY-2001.
XX
PF   01-NOV-2000; 2000WO-US30109.
XX
PR   01-NOV-1999;   99US-0162803.
PR   30-JUN-2000; 2000US-0215564.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Attie AD,  Cook M,  Gray-Keller MP,  Hayden MR,  Pimstone S;
PI   Brooks-Wilson A;
XX
DR   WPI; 2001-335779/35.
DR   P-PSDB; AAB62691.
XX
PT   New method for inhibiting cholesterol uptake in the gut comprises
PT   administration of an inhibitor of an ABC1 protein
XX
PS   Disclosure; Page 34-36; 41pp; English.
XX
CC   The invention relates to a new method for inhibiting cholesterol uptake
CC   in the gut that comprises administration of an inhibitor of an ABC1
CC   protein. The method is useful for: lowering levels of LDL (low density
CC   lipoprotein) cholesterol by reducing the activity of ABC1 protein in the
CC   intestinal cells and the abundance of the ABC1 protein in the individual
CC   by inhibiting the activity of the protein; identifying drugs that can
CC   lower serum cholesterol and LDL levels comprises assaying the drug to
CC   test if it can bind to an ABC1 protein; testing LDL cholesterol lowering
CC   agents; and for modulation of ABC1 biological activity. The present
CC   sequence represents a human ABC1 nucleotide sequence.
XX
SQ   Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;

  Query Match             97.8%;  Score 490;  DB 22;  Length 7860;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-126;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7034 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7093

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7094 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7153

Qy     121 TTGAACTCACAC-TTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 179
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    7154 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAA 7213

Qy     180 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7214 TAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATC 7273

Qy     240 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7274 CTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCT 7333

Qy     300 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7334 GGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGG 7393

Qy     360 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7394 TGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCA 7453

Qy     420 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7454 GTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGT 7513

Qy     480 TCTGGTGGCAGTAACATGCAAC 501
           |||||||||||||||||||||
Db    7514 TCTGGTGGCAGTAACATGCAAC 7535


Search completed: April  3, 2003, 13:38:12
Job time : 140.452 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 Seconds
(without alignments)
11152.306 Million cell updates/sec

Title: US-09-595-526C-1_COPY_7250_7750
Perfect score: 501
Sequence: 1 ttacaggggcagtgcctttg.....tggtggcagtaacatgcaac 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	35	7.0	4010	5	PCT-US94-07297-40	Sequence 40, Appl
c	2	34.8	6.9	2378	4	US-08-802-805D-20	Sequence 20, Appl
	3	34.8	6.9	169998	4	US-09-676-610B-24	Sequence 24, Appl
	4	34.6	6.9	945	4	US-09-134-001C-415	Sequence 415, App
c	5	34.4	6.9	748	1	US-08-361-467B-3	Sequence 3, Appli
c	6	34.4	6.9	748	1	US-08-484-332C-3	Sequence 3, Appli
c	7	34.2	6.8	681	4	US-09-134-001C-741	Sequence 741, App
c	8	34	6.8	7351	1	US-08-224-391-83	Sequence 83, Appl
c	9	34	6.8	7351	1	US-08-484-304-83	Sequence 83, Appl
c	10	34	6.8	7351	2	US-08-184-009-127	Sequence 127, App
c	11	34	6.8	7351	2	US-08-566-398-39	Sequence 39, Appl
c	12	34	6.8	7351	2	US-08-458-356-127	Sequence 127, App
c	13	34	6.8	7351	2	US-08-658-665-39	Sequence 39, Appl
c	14	34	6.8	7351	4	US-08-796-101-3	Sequence 3, Appli
c	15	34	6.8	7351	4	US-08-460-736-127	Sequence 127, App
c	16	34	6.8	7351	4	US-09-085-273-39	Sequence 39, Appl
	17	33.8	6.7	4526	1	US-07-855-412B-4	Sequence 4, Appli
	18	33.8	6.7	4526	2	US-08-308-887A-4	Sequence 4, Appli
	19	33.8	6.7	4526	3	US-08-881-094-4	Sequence 4, Appli
c	20	33.4	6.7	8920	2	US-08-446-855A-1	Sequence 1, Appli
c	21	33.4	6.7	8920	4	US-09-150-741-1	Sequence 1, Appli
	22	33	6.6	2193	4	US-09-427-261-2	Sequence 2, Appli
	23	33	6.6	2193	4	US-09-427-261-3	Sequence 3, Appli
c	24	32.8	6.5	609	1	US-08-268-072-2	Sequence 2, Appli
c	25	32.8	6.5	609	4	US-08-690-721-2	Sequence 2, Appli
c	26	32.4	6.5	1651	4	US-09-465-558-49	Sequence 49, Appl
c	27	32.2	6.4	114	1	US-08-120-827-99	Sequence 99, Appl
c	28	32.2	6.4	114	1	US-08-478-675-99	Sequence 99, Appl
c	29	32	6.4	740	2	US-08-713-000-8	Sequence 8, Appli
c	30	32	6.4	740	2	US-08-975-316-8	Sequence 8, Appli
c	31	32	6.4	740	4	US-09-211-710-8	Sequence 8, Appli
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c	33	32	6.4	741	2	US-08-975-316-58	Sequence 58, Appl
c	34	32	6.4	741	4	US-09-615-192A-58	Sequence 58, Appl
c	35	32	6.4	788	4	US-09-615-192A-96	Sequence 96, Appl
	36	32	6.4	3167	4	US-09-276-531-132	Sequence 132, App
c	37	32	6.4	4668	4	US-09-045-301-1	Sequence 1, Appli
	38	31.8	6.3	2196	1	US-08-090-523-29	Sequence 29, Appl
	39	31.8	6.3	2196	1	US-08-334-639-1	Sequence 1, Appli
	40	31.8	6.3	2196	1	US-08-398-627-29	Sequence 29, Appl
	41	31.8	6.3	2196	1	US-08-406-858-24	Sequence 24, Appl
	42	31.8	6.3	2196	5	PCT-US94-05275-24	Sequence 24, Appl
c	43	31.8	6.3	2700	3	US-09-315-861-1	Sequence 1, Appli
c	44	31.8	6.3	2700	4	US-09-398-395A-43	Sequence 43, Appl
c	45	31.8	6.3	3083	2	US-08-480-994-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
PCT-US94-07297-40/c
; Sequence 40, Application PC/TUS9407297
; GENERAL INFORMATION:
; APPLICANT: Arai, Naoko
; APPLICANT: Masuda, Esteban S.
; APPLICANT: Tokumitsu, Hiroshi
; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
; TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. C. Blasdale, Schering-Plough Corporation, M-3-W
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh IIci
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07297
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/222,626
; FILING DATE: 04-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,061
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/113,971
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,998
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/088,483
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasdale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: DX0392K4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7398
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  4010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  304..3531
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  replace(1756..1758, "gta")
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  replace(1756..1758, "gaa")
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;      LOCATION:  replace(3090..3092, "agg")
PCT-US94-07297-40

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  Best Local Similarity   51.6%;  Pred. No. 0.6;
  Matches   80;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy     133 TTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAATAATTCATCAAGT 192
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Db    3994 TTGTTTTCTTTTTTTTTCTTTTTTTTTTTTTTTTGGGGTTCTAGAAGGTCTTATCAAAA 3935

Qy     193 AATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCCTCATTCACTAAG 252
             || |        | |  | || ||||  ||  ||   | || ||   ||| |  |
Db    3934 GTTCCTATTTTAAAAATTATCATAAAAACTAAGGGGCCCTTCAAATGACCATAAAGCAGT 3875

Qy     253 CCATGCCATGCCCAGGAGACTGGTTTCCCGGTGAC 287
           ||   ||   |    ||    ||  || ||| ||
Db    3874 ACAAATCACCACTCCTAGTTAAGTAACCAGGTCAC 3840


RESULT 2
US-08-802-805D-20/c
; Sequence 20, Application US/08802805D
; Patent No. 6372453
;  GENERAL INFORMATION:
;    APPLICANT:  Robert D. Klein
;    TITLE OF INVENTION:  Neurturin Receptor
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,805D
;      FILING DATE:  18-Feb-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P1086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-8674
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2378 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-802-805D-20

  Query Match             6.9%;  Score 34.8;  DB 4;  Length 2378;
  Best Local Similarity   53.7%;  Pred. No. 0.56;
  Matches   72;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy     133 TTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAATAATTCATCAAGT 192
           ||||||||||||||| ||  | | | || |  ||     || || || | || ||
Db    2289 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGTGTAAGAAGAGTTGATTTTCA 2230

Qy     193 AATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCCTCATTCACTAAG 252
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Db    2229 GCTACATTCAGCTTCTCACTCAAGCAAAGCTCAGGAGAGTGCCCATCAACAATCCGGGAG 2170

Qy     253 CCATGCCATGCCCA 266
           |  ||||| | |||
Db    2169 CTGTGCCAGGGCCA 2156


RESULT 3
US-09-676-610B-24
; Sequence 24, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
;  FILE REFERENCE: RTS-0138
;  CURRENT APPLICATION NUMBER: US/09/676,610B
;  CURRENT FILING DATE:  2000-09-29
;  NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 24
;   LENGTH: 169998
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1208)...(1472)
;   NAME/KEY: intron
;   LOCATION: (1473)...(124390)
;   NAME/KEY: exon
;   LOCATION: (124391)...(124544)
;   NAME/KEY: intron
;   LOCATION: (124545)...(125409)
;   NAME/KEY: exon
;   LOCATION: (125410)...(125595)
;   NAME/KEY: intron
;   LOCATION: (125596)...(128711)
;   NAME/KEY: exon
;   LOCATION: (128712)...(128848)
;   NAME/KEY: intron
;   LOCATION: (128849)...(133400)
;   NAME/KEY: exon
;   LOCATION: (133401)...(133469)
;   NAME/KEY: intron
;   LOCATION: (133470)...(134652)
;   NAME/KEY: exon
;   LOCATION: (134653)...(134773)
;   NAME/KEY: intron
;   LOCATION: (134774)...(136116)
;   NAME/KEY: exon
;   LOCATION: (136117)...(136261)
;   NAME/KEY: intron
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;   LOCATION: (136262)...(137936)
;   NAME/KEY: exon
;   LOCATION: (137937)...(138053)
;   NAME/KEY: intron
;   LOCATION: (138054)...(138637)
;   NAME/KEY: exon
;   LOCATION: (138638)...(138766)
;   NAME/KEY: intron
;   LOCATION: (138767)...(138864)
;   NAME/KEY: exon
;   LOCATION: (138865)...(138940)
;   NAME/KEY: intron
;   LOCATION: (138941)...(139765)
;   NAME/KEY: exon
;   LOCATION: (139766)...(139860)
;   NAME/KEY: intron
;   LOCATION: (139861)...(142245)
;   NAME/KEY: exon
;   LOCATION: (142246)...(142445)
;   NAME/KEY: intron
;   LOCATION: (142446)...(143605)
;   NAME/KEY: exon
;   LOCATION: (143606)...(143738)
;   NAME/KEY: intron
;   LOCATION: (143739)...(145838)
;   NAME/KEY: exon
;   LOCATION: (145839)...(145931)
;   NAME/KEY: intron
;   LOCATION: (145932)...(147385)
;   NAME/KEY: exon
;   LOCATION: (147386)...(147544)
;   NAME/KEY: intron
;   LOCATION: (147545)...(153274)
;   NAME/KEY: exon
;   LOCATION: (153275)...(153321)
;   NAME/KEY: intron
;   LOCATION: (153322)...(155088)
;   NAME/KEY: exon
;   LOCATION: (155089)...(155231)
;   NAME/KEY: intron
;   LOCATION: (155232)...(156025)
;   NAME/KEY: exon
;   LOCATION: (156026)...(156151)
;   NAME/KEY: intron
;   LOCATION: (156152)...(156826)
;   NAME/KEY: exon
;   LOCATION: (156827)...(156928)
;   NAME/KEY: intron
;   LOCATION: (156929)...(163399)
;   NAME/KEY: exon
;   LOCATION: (163400)...(163586)
US-09-676-610B-24

  Query Match             6.9%;  Score 34.8;  DB 4;  Length 169998;
  Best Local Similarity   60.6%;  Pred. No. 3;
  Matches   57;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy    104 CCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTC 163
          |||| |  || |    |  |   |   | || |||||||| |||||||| || ||||||
Db 168633 CCAAGGACCAGAGATTTCAGTTATGTGAGTTATTTTTTTTATTTGTTCTTGCGTATTCCA 168692

Qy    164 ATTGGGGTTGCAACAATAATTCATCAAGTAATCA 197
              |||| ||| | | | || | | | | ||||
Db 168693 CAAAGGGTCGCAGCTAAACTTAACCTAATGATCA 168726


RESULT 4
US-09-134-001C-415
; Sequence 415, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 415
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-415

  Query Match             6.9%;  Score 34.6;  DB 4;  Length 945;
  Best Local Similarity   49.7%;  Pred. No. 0.44;
  Matches   88;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy    189 AAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCCTCATTCAC 248
          || || || |    | | |  |||  ||||||||||| |  ||     |   |   |  |
Db    228 AACTACTCGTATTAAACAAGCATTTTTCAAAATCAAAGGCGAAACACGAAATTGTATTGC 287

Qy    249 TAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTGGCAATGAG 308
          |  | |    | |  ||  | ||||  |||  |  |    |||   | | | | | |
Db    288 AATACTACATGAAGGACAACAAACTGAAATCCTTGAAAAGGGTCCCACGATTGAACTTAA 347

Qy    309 TGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGTGTGTC 365
          |   |||||  |||   | ||  | | | | ||  ||| ||  |   || |||| |
Db    348 GGAATCAGAGGAATTCAAGTCACATCTATTAAAACTTTTCAAAGAAACTGATGTGGC 404


RESULT 5
US-08-361-467B-3/c
; Sequence 3, Application US/08361467B
; Patent No. 5633441
;  GENERAL INFORMATION:
;    APPLICANT:  De Greef, Willy
;    APPLICANT:  Van Emmelo, John
;    APPLICANT:  De Oliveria, Dulce E.
;    APPLICANT:  De Souza, Maria-Helena
;    APPLICANT:  Van Montagu, Marc
;    TITLE OF INVENTION:  PLANTS WITH MODIFIED FLOWERS, SEEDS OR
;    TITLE OF INVENTION:  EMBRYOS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/361,467B
;      FILING DATE:  22-DEC-1994
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,492
;      FILING DATE:  04-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP90/01275
;      FILING DATE:  01-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 89 402 224.3
;      FILING DATE:  04-AUG-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schulman, Robert M.
;      REGISTRATION NUMBER:  31,196
```

```
;      REFERENCE/DOCKET NUMBER:  010830-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  748 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    IMMEDIATE SOURCE:
;      CLONE:  4B12
US-08-361-467B-3

  Query Match             6.9%;  Score 34.4;  DB 1;  Length 748;
  Best Local Similarity   53.8%;  Pred. No. 0.46;
  Matches   71;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy     112 CATATGGGTTTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGT 171
           ||| |   |||     |     |||||||||||||||| ||  | | | || |  ||    |
Db     746 CATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 687

Qy     172 TGCAACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAA 231
               |    || ||| |    |   ||  | ||| || | | |  | || ||| |   ||
Db     686 ATGTATTCCAAGTCACCTTAAATAGATTACTAGCCATAACTTACTACAAACAACACAGAA 627

Qy     232 TGCACATCCTCA 243
           |||| |||  ||
Db     626 TGCAAATCTCCA 615


RESULT 6
US-08-484-332C-3/c
; Sequence 3, Application US/08484332C
; Patent No. 5767374
;  GENERAL INFORMATION:
;    APPLICANT:  De Greef, Willy
;    APPLICANT:  Van Emmelo, John
;    APPLICANT:  De Oliveria, Dulce E.
;    APPLICANT:  De Souza, Maria-Helena
;    APPLICANT:  Van Montagu, Marc
;    TITLE OF INVENTION:  PLANTS WITH MODIFIED FLOWERS, SEEDS OR
;    TITLE OF INVENTION:  EMBRYOS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,332C
;      FILING DATE:  7-JUNE-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/361,467
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,492
;      FILING DATE:  04-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP90/01275
;      FILING DATE:  01-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 89 402 224.3
;      FILING DATE:  04-AUG-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schulman, Robert M.
;      REGISTRATION NUMBER:  31,196
;      REFERENCE/DOCKET NUMBER:  010830-093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  748 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    IMMEDIATE SOURCE:
;      CLONE:  4B12
US-08-484-332C-3

  Query Match             6.9%;  Score 34.4;  DB 1;  Length 748;
  Best Local Similarity   53.8%;  Pred. No. 0.46;
  Matches   71;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy     112 CATATGGGTTTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGT 171
           ||| |   |||     |     |||||||||||||||| ||  | | | || |  ||    |
Db     746 CATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 687

Qy     172 TGCAACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAA 231
               |    || ||| |    |   ||  | ||| || | | |  | || ||| |   ||
Db     686 ATGTATTCCAAGTCACCTTAAATAGATTACTAGCCATAACTTACTACAAACAACACAGAA 627

Qy     232 TGCACATCCTCA 243
           |||| |||  ||
Db     626 TGCAAATCTCCA 615


RESULT 7
US-09-134-001C-741/c
; Sequence 741, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 741
;   LENGTH: 681
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-741

  Query Match             6.8%;  Score 34.2;  DB 4;  Length 681;
  Best Local Similarity   48.7%;  Pred. No. 0.51;
  Matches   93;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy      55 CTTGAATTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACAT 114
           ||| ||| | | |   ||  |     | | |   | | | || | |||   |     | |
Db     262 CTTTAATATCGATAAATATTTTAGTTTCTTTTGTATTATCTTTTTGAATAGACACTTCTT 203

Qy     115 ATGGGTTTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGC 174
             |   ||| |  |    || |||||| |||  || ||   | | ||    |     |
Db     202 TTTTATTTAACTTTTTGCTATTTTTTATTTGCTGGTCAGATATTTTAGATTGTCTTTCCT 143

Qy     175 AACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGC 234
           || ||  |  ||||| | || || |  | |  | | | |  ||||  | || ||  |
Db     142 GACTATTCTGTATCAAATCATTATTGTTATCATTGAGTAAGTAAAAAAAGAATGTTGTTA 83
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Qy    235 ACATCCTCATT 245
          ||||  | | |
Db     82 ACATTATTAAT 72


RESULT 8
US-08-224-391-83/c
; Sequence 83, Application US/08224391
; Patent No. 5744140
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Pincus, Steven E.
;    TITLE OF INVENTION:  FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/224,391
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/729,800
;      FILING DATE:  17-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-224-391-83

  Query Match             6.8%;  Score 34;  DB 1;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  | ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 9
US-08-484-304-83/c
; Sequence 83, Application US/08484304
; Patent No. 5744141
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Pincus, Steven E.
;    TITLE OF INVENTION:  FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,304
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/224,391
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/729,800
;      FILING DATE:  17-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-484-304-83

  Query Match             6.8%;  Score 34;  DB 1;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  | ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 10
US-08-184-009-127/c
; Sequence 127, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-127

  Query Match             6.8%;  Score 34;  DB 2;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 11
US-08-566-398-39/c
; Sequence 39, Application US/08566398
; Patent No. 5858373
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Gettig, Russell
;    TITLE OF INVENTION:  RECOMBINANT POXVIRUS - FELINE INFECTIOUS
;    TITLE OF INVENTION:  PERITONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR
;    TITLE OF INVENTION:  MAKING AND USING THEM
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/566,398
;      FILING DATE:  01-DEC-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2880
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-566-398-39

  Query Match             6.8%;  Score 34;  DB 2;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
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Db    2517 TT 2516


RESULT 12
US-08-458-356-127/c
; Sequence 127, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
US-08-458-356-127

  Query Match             6.8%;  Score 34;  DB 2;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 13
US-08-658-665-39/c
; Sequence 39, Application US/08658665
; Patent No. 5997878
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Kauffman, Elizabeth K.
;    TITLE OF INVENTION:  Recombinant Poxvirus - Cytomegalovirus,
;    TITLE OF INVENTION:  Compositions and Uses
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,665
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2720.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)840-3333
;      TELEFAX:  (212)840-0712
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-665-39

  Query Match             6.8%;  Score 34;  DB 2;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 14
US-08-796-101-3/c
; Sequence 3, Application US/08796101
; Patent No. 6183752
;  GENERAL INFORMATION:
;    APPLICANT:  EPSTEIN, STEPHEN E.
;    APPLICANT:  FINKEL, TOREN
;    APPLICANT:  SPEIR, EDITH
;    APPLICANT:  ZHOU, YI FU
;    APPLICANT:  ZHU, JIANHUI
;    APPLICANT:  ERDILE, LORNE
;    APPLICANT:  PINCUS, STEVEN
;    TITLE OF INVENTION:  RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
;    TITLE OF INVENTION:  PROPHYLAXIS AND THERAPY
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CURTIS, MORRIS & SAFFORD, P.C.
;      STREET:  530 FIFTH AVENUE
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/796,101
;      FILING DATE:  05-FEB-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOWALSKI, THOMAS J.
;      REGISTRATION NUMBER:  32,147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 764-5574
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-796-101-3

  Query Match             6.8%;  Score 34;  DB 4;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||        |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


RESULT 15
US-08-460-736-127/c
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; Sequence 127, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7351 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-127

  Query Match             6.8%;  Score 34;  DB 4;  Length 7351;
  Best Local Similarity   54.9%;  Pred. No. 1.5;
  Matches   67;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      26 TATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGT 85
           ||| || | ||    | |||  |||| ||  |  ||| ||  || ||| | ||  |||||
Db    2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAAGGGTTATACTTTTAAGTATGT 2578

Qy      86 GAAACTCTATTATGGAACCCAATGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTT 145
             | |||| | ||  || |   |  |  ||         |  |||   |||| | |  |||
Db    2577 TTATCTCTTTAATACAATCATCTTTAATTAATTTGAATATATCATTATTTTCTATAGTTT 2518

Qy     146 TT 147
           ||
Db    2517 TT 2516


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Title: US-09-595-526C-1_COPY_7250_7750
Perfect score: 501
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	501	100.0	2894	9	US-09-984-827-85	Sequence 85, Appl
2	501	100.0	2894	9	US-09-984-827-86	Sequence 86, Appl
3	501	100.0	2894	9	US-09-984-827-87	Sequence 87, Appl
4	501	100.0	2894	9	US-09-984-827-88	Sequence 88, Appl
5	501	100.0	2894	9	US-09-984-827-89	Sequence 89, Appl
6	501	100.0	2894	9	US-09-984-827-90	Sequence 90, Appl
7	501	100.0	2894	9	US-09-984-827-91	Sequence 91, Appl
8	501	100.0	5352	9	US-09-984-827-22	Sequence 22, Appl
9	501	100.0	9741	9	US-09-984-827-1	Sequence 1, Appli
10	501	100.0	9741	10	US-09-846-456-10	Sequence 10, Appl
11	501	100.0	9870	9	US-09-984-827-92	Sequence 92, Appl
12	501	100.0	9870	9	US-09-984-827-93	Sequence 93, Appl
13	501	100.0	9870	9	US-09-984-827-94	Sequence 94, Appl
14	501	100.0	9870	9	US-09-984-827-95	Sequence 95, Appl
15	501	100.0	9870	9	US-09-984-827-96	Sequence 96, Appl
16	501	100.0	9870	9	US-09-984-827-97	Sequence 97, Appl
17	501	100.0	9870	9	US-09-984-827-98	Sequence 98, Appl
18	501	100.0	9870	9	US-09-984-827-99	Sequence 99, Appl
19	501	100.0	9870	9	US-09-984-827-100	Sequence 100, App
20	501	100.0	9870	9	US-09-984-827-101	Sequence 101, App
21	501	100.0	9870	9	US-09-984-827-102	Sequence 102, App
22	501	100.0	9870	9	US-09-984-827-103	Sequence 103, App
23	501	100.0	9870	9	US-09-984-827-104	Sequence 104, App
24	501	100.0	9870	9	US-09-984-827-105	Sequence 105, App
25	501	100.0	9870	9	US-09-984-827-106	Sequence 106, App
26	501	100.0	9870	9	US-09-984-827-107	Sequence 107, App
27	501	100.0	9870	9	US-09-984-827-108	Sequence 108, App
28	501	100.0	9870	9	US-09-984-827-109	Sequence 109, App
29	501	100.0	9870	9	US-09-984-827-110	Sequence 110, App
30	501	100.0	9870	9	US-09-984-827-111	Sequence 111, App
31	501	100.0	9870	9	US-09-984-827-112	Sequence 112, App
32	501	100.0	9870	9	US-09-984-827-113	Sequence 113, App
33	501	100.0	9870	9	US-09-984-827-114	Sequence 114, App
34	501	100.0	9870	9	US-09-984-827-115	Sequence 115, App
35	501	100.0	9870	9	US-09-984-827-116	Sequence 116, App
36	501	100.0	9870	9	US-09-984-827-117	Sequence 117, App
37	501	100.0	9870	9	US-09-984-827-118	Sequence 118, App
38	501	100.0	9870	9	US-09-984-827-120	Sequence 120, App
39	501	100.0	9870	9	US-09-984-827-121	Sequence 121, App
40	501	100.0	9870	9	US-09-984-827-122	Sequence 122, App
41	501	100.0	9870	9	US-09-984-827-123	Sequence 123, App
42	501	100.0	9870	9	US-09-984-827-124	Sequence 124, App
43	501	100.0	9870	9	US-09-984-827-125	Sequence 125, App
44	501	100.0	9870	9	US-09-984-827-126	Sequence 126, App
45	499.4	99.7	2894	9	US-09-984-827-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-984-827-85
; Sequence 85, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-85

Query Match 100.0%; Score 501; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 8.5e-135;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db     315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy      61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db     375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434
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Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
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Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db    795 CTGGTGGCAGTAACATGCAAC 815
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RESULT 2
US-09-984-827-86
; Sequence 86, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-86

Query Match 100.0%; Score 501; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 8.5e-135;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434
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Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Db    435 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815
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RESULT 3
US-09-984-827-87
; Sequence 87, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-87

Query Match 100.0%; Score 501; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 8.5e-135;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
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Db    435 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815


RESULT 4
US-09-984-827-88
; Sequence 88, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 2894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (180)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-88

  Query Match            100.0%;  Score 501;  DB 9;  Length 2894;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-135;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815


RESULT 5
US-09-984-827-89
; Sequence 89, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 2894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (180)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-89

  Query Match            100.0%;  Score 501;  DB 9;  Length 2894;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-135;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494
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Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815
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RESULT 6
US-09-984-827-90
; Sequence 90, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
;   LENGTH: 2894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (180)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-90

  Query Match           100.0%;  Score 501;  DB 9;  Length 2894;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-135;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494
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Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815
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RESULT 7
US-09-984-827-91
; Sequence 91, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 2894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (180)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-91

  Query Match           100.0%;  Score 501;  DB 9;  Length 2894;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-135;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 374

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 434

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 494

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
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Db    495 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 554

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 734

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 794

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    795 CTGGTGGCAGTAACATGCAAC 815
```

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RESULT 8
US-09-984-827-22
; Sequence 22, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 5352
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (374)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-22

  Query Match           100.0%;  Score 501;  DB 9;  Length 5352;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 568

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 628

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 TTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 688

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 748

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 808

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 868

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 928

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 988

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db    989 CTGGTGGCAGTAACATGCAAC 1009
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```
RESULT 9
US-09-984-827-1
; Sequence 1, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9741
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7009)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-1

  Query Match           100.0%;  Score 501;  DB 9;  Length 9741;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383
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```
Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 10
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
;  APPLICANT: Rosier, Marie
;  APPLICANT:  Prades, Catherine
;  APPLICANT:  Lemoine, Cendrine
;  APPLICANT:  Naudin, Laurent
;  APPLICANT:  Denefle, Patrice
;  APPLICANT:  Duverger, Nicolas
;  APPLICANT:  Brewer, Bryan
;  APPLICANT:  Remaley, Alan
;  APPLICANT:  Fojo, Silvia
;  TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
;  TITLE OF INVENTION:  Activity and Therapeutic Uses
;  FILE REFERENCE: 3806.0505
;  CURRENT APPLICATION NUMBER: US/09/846,456
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,280
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 9741
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

  Query Match           100.0%;  Score 501;  DB 10;  Length 9741;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7144 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7203

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7204 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7263

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7264 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7323

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7324 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7383

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7384 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7443

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7503

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7504 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7564 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7623

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7624 CTGGTGGCAGTAACATGCAAC 7644


RESULT 11
US-09-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-92

  Query Match           100.0%;  Score 501;  DB 9;  Length 9870;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7273 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7332

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7333 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7392

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7393 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7452

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7453 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7512
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Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7513 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7572

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7633 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7692

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7693 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7752

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7753 CTGGTGGCAGTAACATGCAAC 7773
```

```
RESULT 12
US-09-984-827-93
; Sequence 93, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-93

  Query Match             100.0%;  Score 501;  DB 9;  Length 9870;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7273 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7332

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7333 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7392

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7393 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7452

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7453 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7512

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7513 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7572

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7633 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7692

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7693 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7752

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7753 CTGGTGGCAGTAACATGCAAC 7773
```

```
RESULT 13
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
;  APPLICANT: DENEFLE, PATRICE
;  APPLICANT:  ROSIER-MONTUS, MARIE-FRANCOISE
;  APPLICANT:  ARNOULD-REGUIGNE, ISABELLE
;  APPLICANT:  DUVERGER, NICOLAS
;  APPLICANT:  CAMBIEN, FRANCOIS
;  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
;  TITLE OF INVENTION:  DETECTION METHODS AND KITS THEREFOR
;  FILE REFERENCE: 03806.0522-00000
;  CURRENT APPLICATION NUMBER: US/09/984,827
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 60/254,108
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: FR 00/14037
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
;   LENGTH: 9870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7138)
;   OTHER INFORMATION: a, t, c or g
US-09-984-827-94

  Query Match             100.0%;  Score 501;  DB 9;  Length 9870;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-134;
  Matches  501;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7273 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7332

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7333 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7392

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7393 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7452

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7453 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7512

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   7513 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7572

Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7633 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7692

Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7693 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7752

Qy    481 CTGGTGGCAGTAACATGCAAC 501
          |||||||||||||||||||||
Db   7753 CTGGTGGCAGTAACATGCAAC 7773
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RESULT 14
US-09-984-827-95
; Sequence 95, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-95

Query Match 100.0%; Score 501; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db   7273 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7332

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db   7333 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7392

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7393 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7452

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7453 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7512

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Db   7513 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7572
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Qy    301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
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Db   7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632

Qy    361 GTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420
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Qy    421 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 480
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Db   7693 TTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCCTCTGATAAGCTGTT 7752

Qy    481 CTGGTGGCAGTAACATGCAAC 501
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Db   7753 CTGGTGGCAGTAACATGCAAC 7773
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RESULT 15
US-09-984-827-96
; Sequence 96, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-96

Query Match 100.0%; Score 501; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 60
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Db   7273 TTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAGTGAAAGACTTGAA 7332

Qy     61 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 120
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Db   7333 TTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAATGGACATATGGGT 7392

Qy    121 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7393 TTGAACTCACACTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATTGGGGTTGCAACAAT 7452

Qy    181 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7453 AATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAAGGTAATGCACATCC 7512

Qy    241 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300
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Db   7513 TCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 7572
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